GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: Octoher 20, 2005, 05:59:01 ; Search time 17 Seconds
(without alignments)
2190.346 Million cell updates/sec

Title: US-10-800-249-2
Perfect score: 2081
Sequence: 1 MNRHHLQDHFLEIDKKNCCV.....KGHCHQEPASLEKQLGCCIE 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1990	95.6	387	2	I69202	G protein-coupled
2	431	20.7	362	2	S33733	G protein-coupled
3	415	19.9	373	2	JC4162	P2Y receptor - bov
4	407	19.6	373	2	JC4737	G protein-coupled
5	351.5	16.9	308	2	I50241	G protein-coupled
6	350.5	16.8	364	2	JQ1488	bradykinin B2 rece
7	348.5	16.7	370	2	JC5549	heptahelical P2Y5-
8	348	16.7	328	2	I55450	G protein-coupled
9	341	16.4	399	2	I48705	proteinase activat
10	339.5	16.3	344	2	T09508	intron 17 purinerg
11	337	16.2	373	2	A47556	ATP receptor P2u -
12	337	16.2	397	2	S66518	proteinase-activat
13	333	16.0	342	2	A40191	platelet-activatin
14	330.5	15.9	384	2	A47249	brain-specific som
15	326.5	15.7	366	1	OORTB2	bradykinin recepto
16	326	15.7	380	2	JC2338	kappa opioid recep
17	325	15.6	380	2	A55259	kappa opioid recep
18	324.5	15.6	380	2	S36143	kappa opioid recep
19	323	15.5	328	2	JC4800	P2Y6 receptor - hu
20	323	15.5	365	2	S68679	G protein-coupled
21	323	15.5	425	2	A37912	thrombin receptor
22	322.5	15.5	380	2	A48227	kappa opioid recep
23	322	15.5	388	2	JN0605	somatostatin recep
24	321	15.4	420	2	I51667	thrombin receptor
25	320	15.4	366	2	I49519	bradykinin B2 rece
26	317	15.2	369	2	JC5068	G protein-coupled
27	317	15.2	391	2	C41795	somatostatin recep
28	317	15.2	391	2	A39297	somatostatin recep
29	316	15.2	391	2	A41795	somatostatin recep
30	315.5	15.2	369	2	B41795	somatostatin recep
31	314.5	15.1	342	2	S13638	platelet-activatin
32	314.5	15.1	369	2	JC2083	somatostatin recep
33	314.5	15.1	380	2	JC2434	kappa opioid recep
34	314.5	15.1	384	2	JC4629	somatostatin recep
35	313.5	15.1	369	2	A45291	somatostatin recep
36	313.5	15.1	432	2	A43448	thrombin receptor
37	310	14.9	341	2	S63666	platelet activatin
38	310	14.9	341	2	S43252	platelet-activatin
39	309	14.8	398	2	A57510	mu opioid receptor
40	308.5	14.8	398	2	I56517	mu opioid receptor
41	307.5	14.8	364	2	JN0763	somatostatin recep
42	307	14.8	418	2	A46226	somatostatin recep
43	306	14.7	355	2	I49339	macrophage inflamm
44	305.5	14.7	372	2	I38532	delta opioid recep
45	305	14.7	355	2	A45177	chemokine (C-C) re

ALIGNMENTS

RESULT 1
I69202
G protein-coupled receptor HM74 - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I69202
R;Nomura, H.; Nielsen, B.W.; Matsushima, K.
Int. Immunol. 5, 1239-1249, 1993
A;Title: Molecular cloning of cDNAs encoding a LD78 receptor and putative leukocyte chem
A;Reference number: I54751; MUID:94092629; PMID:7505609
A;Accession: I69202
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-387 <RES>
A;Cross-references: UNIPROT:P49019; GB:D10923; NID:g219866; PIDN:BAA01721.1; PID:g219867
C;Genetics:
A;Gene: HM74
C;Superfamily: G protein-coupled receptor 4

Query Match 95.6%; Score 1990; DB 2; Length 387;
Best Local Similarity 95.9%; Pred. No. 3.6e-170;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

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Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              ||||||||||||||||||||:|| |||| || |||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:|||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
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RESULT 2
S33733
G protein-coupled receptor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S33733
R;Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstoc
FEBS Lett. 324, 219-225, 1993
A;Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A;Reference number: S33733; MUID:93285340; PMID:8508924
A;Accession: S33733
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <WEB>
A;Cross-references: UNIPROT:P34996; EMBL:X73268; NID:g395084; PIDN:CAA51716.1; PID:g3950
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 20.7%; Score 431; DB 2; Length 362;
Best Local Similarity 30.7%; Pred. No. 7.9e-31;
Matches 101; Conservative 68; Mismatches 134; Indels 26; Gaps 7;

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Qy         18 CCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLI 77
              | : :  |    || |  | || | ||| :|:|:| ||:: |    :::||||:|||| :
Db         31 CSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLYV 90

Qy         78 ICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALN 137
              : || |:  |  : || |||: |:|  |:  :|  |||:||| ::| ||  |||  :|
Db         91 LTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTGVVHPLKSLG 150

Qy        138 KISNRTAAIISCLLWGITIGLTVHLL---------KKKMPIQNGGAN--LCSSF--SICH 184
              ::  : |  :| |:| : : :   :|          | :   :  |:  | | |  |:|
Db        151 RLKKKNAVYVSSLVWALVVAVIAPILFYSGTGVRRNKTITCYDTTADEYLRSYFVYSMCT 210

Qy        185 TFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICF 244
              |       :  | :|  :|| |   |: :|  : :|     :::|  :::|  || : :
Db        211 T--------VFMFCIPFIVILGCYGLIVKALIYKDLDNSPLRRKSIYLVIIVLTVFAVSY 262

Qy        245 LPSVVVR-IRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPN 303
              ||  |:: : :   |     | |     |   : :|     :|| :||::|: :  :|
Db        263 LPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFRR 322

Qy        304 FFSTLINRCLQRKMTGEPDNNRSTSVELT 332
                |    :  :|    || | :| | |:|
Db        323 RLSRATRKSSRR---SEP-NVQSKSEEMT 347
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RESULT 3
JC4162
P2Y receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 12-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: JC4162
R;Henderson, D.J.; Elliot, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.
Biochem. Biophys. Res. Commun. 212, 648-656, 1995
A;Title: Cloning and characterisation of a bovine P2Y receptor.
A;Reference number: JC4162; MUID:95352058; PMID:7626079
A;Accession: JC4162
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
A;Cross-references: UNIPROT:P48042; EMBL:X87628; NID:g1032484; PIDN:CAA60958.1; PID:g103
A;Experimental source: aortic endothelial cell
C;Genetics:
A;Gene: bovp2y
C;Superfamily: ATP receptor P2u
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;52-77/Domain: transmembrane #status predicted <TM1>
F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-150/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 19.9%; Score 415; DB 2; Length 373;
Best Local Similarity 29.8%; Pred. No. 2.2e-29;
Matches 98; Conservative 66; Mismatches 139; Indels 26; Gaps 6;

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Qy         18 CCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLI 77
              | : :  |    || |  | || | ||| :|:|:| ||:| |    :::||||:|||| :
Db         42 CALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYV 101

Qy         78 ICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALN 137
              : || |:  |  : || |||  |:|  |:  :|  |||:||| ::  ||  ||:|  :|
Db        102 LTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLG 161

Qy        138 KISNRTAAIISCLLWGI-TIGLTVHLLKKKMPIQNGGANLCSS----------FSICH 184
              ::  : |  || |:| |  :|::  |       |:       |             :|:|
Db        162 RLKKKNAVYISVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSMCT 221

Qy        185 TFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICF 244
              |      |||     :|| :|| | |: :|  : :|     :::|  :::|  || : :
Db        222 TV----AMFC----VPLVLILGCYGLIVRALIYKDLDNSPLRRKSIYLVIIVLTVFAVSY 273

Qy        245 LPSVVVR-IRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPN 303
              :|  |:: : :   |     : |     |   : :|     :|| :||::|: :  :|
Db        274 IPFHVMKTMNLRARLDFQTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR 333

Qy        304 FFSTLINRCLQRKMTGEPDNNRSTSVELT 332
                |    :  :|       | :| | ::|
Db        334 RLSRATRKASRRSEA----NLQSKSEDMT 358
```

RESULT 4
JC4737
G protein-coupled receptor P2Y1 - human
N;Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C;Species: Homo sapiens (man)
C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: JC4737; JC4615; S54253
R;Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A;Title: Cloning and tissue distribution of the human P2Y1 receptor.
A;Reference number: JC4737; MUID:96205320; PMID:8630005
A;Accession: JC4737
A;Molecule type: DNA
A;Residues: 1-373 <JAN>
A;Cross-references: UNIPROT:P47900; GB:S81950; NID:g1839438; PIDN:AAB47091.1; PID:g183941
R;Ayyanathan, K.; Webbs, T.E.; Sandhu, A.K.; Athwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A;Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A;Reference number: JC4615; MUID:96158962; PMID:8579591
A;Accession: JC4615
A;Molecule type: mRNA
A;Residues: 1-373 <AYY>
A;Cross-references: GB:U42029; NID:g1147730; PIDN:AAA97872.1; PID:g1147731
A;Experimental source: erythro leukemia cells
R;Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning of a human putative P2Y receptor.
A;Reference number: S54253
A;Accession: S54253
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,139-373 <LEO>
A;Cross-references: EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PID:g798836
C;Comment: This receptor belongs to a family of G protein-coupled receptors. It responds
C;Genetics:
A;Gene: p2Y1; GDB:P2RY1
A;Cross-references: GDB:677125; OMIM:601167
A;Map position: 3pter-3qter
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prote
F;52-77/Domain: transmembrane #status predicted <TM1>

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F;88-111/Domain: transmembrane #status predicted <TM2>
F;124-152/Domain: transmembrane #status predicted <TM3>
F;171-191/Domain: transmembrane #status predicted <TM4>
F;214-237/Domain: transmembrane #status predicted <TM5>
F;261-282/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;11,27,113,197/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;258,336/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predict
F;330,339/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predict
F;343/Binding site: phosphate (Ser) (covalent) (by protein kinase C and calmodulin-deper

  Query Match           19.6%;  Score 407;  DB 2;  Length 373;
  Best Local Similarity  28.5%;  Pred. No. 1.1e-28;
  Matches   97;  Conservative   62;  Mismatches  133;  Indels   48;  Gaps    7;

Qy         18 CCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLI 77
              | : :  |    || |  | || | ||| :|:|:| ||:| |    :::|||||:|||| :
Db         42 CALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYV 101

Qy         78 ICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALN 137
              : || |:  |  : || |||  |:|  |:  :|  |||:||| ::  ||  ||:|  :|
Db        102 LTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLG 161

Qy        138 KISNRTAAIISCLLWGI-TIGLTVHLLKKKMPIQNGGANLCSS------------FSICH 184
              ::  : |  || |:| | : :: |      ::      |                :|:|
Db        162 RLKKKNAICISVLVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSMCT 221

Qy        185 TFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICF 244
              |     |||     :|| :|| |   |: :|  : :|     :::|  :::|  || : :
Db        222 TV----AMFC----VPLVLILGCYGLIVRALIYKDLDNSPLRRKSIYLVIIVLTVFAVSY 273

Qy        245 LPSVVVRIRIFWLLHTSGTQN------------CEVYRSVDLAFFITLSFTYMNSMLDPV 292
              :|           |   | |            |      |   : :|     :|| :||:
Db        274 IP-----------FHVMKTMNLRARLDFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPI 322

Qy        293 VYYFSSPSFPNFFSTLINRCLQRKMTGEPDNNRSTSVELT 332
              :|: :  :|    |    :  :|       | :| | ::|
Db        323 LYFLAGDTFRRRLSRATRKASRRSEA----NLQSKSEDMT 358


RESULT 5
I50241
G protein-coupled receptor 6H1 - chicken
N;Alternate names: purinoceptor 6H1
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50241; JC4618
R;Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A;Title: Identification of a G protein coupled receptor induced in activated T cells.
A;Reference number: I50241; MUID:93329058; PMID:8393036
A;Accession: I50241
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-308 <KAP>
A;Cross-references: UNIPROT:P32250; GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
R;Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A;Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A;Reference number: JC4618; MUID:96190677; PMID:8619790
A;Accession: JC4618
A;Molecule type: mRNA
A;Residues: 1-308 <WEB>
A;Cross-references: GB:L06109; NID:g304383; PIDN:AAB06587.1; PID:g304384
A;Experimental source: T-cells
C;Comment: This receptor plays a role in T-cell activation.
C;Genetics:
A;Gene: p2Y5
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;15-40/Domain: transmembrane #status predicted <TM1>
F;51-74/Domain: transmembrane #status predicted <TM2>
F;89-109/Domain: transmembrane #status predicted <TM3>
F;133-153/Domain: transmembrane #status predicted <TM4>
F;177-201/Domain: transmembrane #status predicted <TM5>
F;227-248/Domain: transmembrane #status predicted <TM6>
F;269-292/Domain: transmembrane #status predicted <TM7>

  Query Match           16.9%;  Score 351.5;  DB 2;  Length 308;
  Best Local Similarity  30.7%;  Pred. No. 8.5e-24;
  Matches   89;  Conservative   59;  Mismatches  129;  Indels   13;  Gaps    9;

Qy         19 CVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLII 78
              |  | |   :   |  : |: ||: | :|::|| | ||    :  :: |||::| | :
Db          6 CSTEDSFKYTLYGCVFSMVFVLGLIANCVAIYIFTFTLKVRNETTTYMLNLAISDLLFVF 65

Qy         79 CLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNK 138
              ||| :  :| | :| |||: |:: : :   |  |||:||| ::|||:  :|||  :
Db         66 TLPFRIYYFVVR-NWPFGDVLCKISVTLFYTNMYGSILFLTCISVDRFLAIVHPFRSKTL 124

Qy        139 ISNRTAAIISCLLWGITI--GLTVHLLKKKMPIQNG-GANLC-SSF--SICHTFQWHEAM 192
              : | | |:   :| ||:  | |     :    ||      |  :|  |   |:     :
Db        125 RTKRNARIVCVAVW-ITVLAGSTPASFFQSTNRQNNTEQRTCFENFPESTWKTYLSRIVI 183

Qy        193 F--LLEFFLPLGIILFCSARIIWSLRQRQMDRHAKI--KRAITFIMVVAIVFVICFLPSV 248
              |  :: ||:|| : : ||  :: :| :       |:  |: :  | |  ::|  ||:|
Db        184 FIEIVGFFIPLILNVTCSTMVLRTLNKPLTLSRNKLSKKKVLKMIFVHLVIFCFCFVPYN 243

Qy        249 VVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSS 298
              :  | :: |: |     || |  :|   : :||     |   ||:||||:|
Db        244 ITLI-LYSLMRTQTWINCSVVTAVRTMYPVTLCIAVSNCCFDPIVYYFTS 292


RESULT 6
JQ1488
bradykinin B2 receptor - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: JH0712; A46022; A55559; JQ1488; JC1400
R;Eggerickx, D.; Raspe, E.; Bertrand, D.; Vassart, G.; Parmentier, M.
Biochem. Biophys. Res. Commun. 187, 1306-1313, 1992
A;Title: Molecular cloning, functional expression and pharmacological characterization o
A;Reference number: JH0712; MUID:93038601; PMID:1329734
A;Accession: JH0712
A;Molecule type: DNA
A;Residues: 1-364 <EGG>
A;Cross-references: UNIPROT:P30411; GB:S45489; NID:g256536; PIDN:AAB23467.1; PID:g256537
R;Powell, S.J.; Slynn, G.; Thomas, C.; Hopkins, B.; Briggs, I.; Graham, A.
Genomics 15, 435-438, 1993
A;Title: Human bradykinin B2 receptor: nucleotide sequence analysis and assignment to ch
A;Reference number: A46022; MUID:93194199; PMID:7916737
A;Accession: A46022
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-364 <POW>
A;Cross-references: GB:S56772; NID:g298604; PIDN:AAB25765.1; PID:g298605
A;Note: sequence extracted from NCBI backbone (NCBIN:127280, NCBIP:127284)
R;Ma, J.; Wang, D.; Ward, D.C.; Chen, L.; Dessai, T.; Chao, J.; Chao, L.
Genomics 23, 362-369, 1994
A;Title: Structure and chromosomal localization of the gene (BDKRB2) encoding human brad
A;Reference number: A55559; MUID:95137582; PMID:7835885
A;Accession: A55559
A;Molecule type: DNA
A;Residues: 1-364 <MAA>
A;Cross-references: GB:L27594
R;Hess, J.F.; Borkowski, J.A.; Young, G.S.; Strader, C.D.; Ransom, R.W.
Biochem. Biophys. Res. Commun. 184, 260-268, 1992
A;Title: Cloning and pharmacological characterization of a human bradykinin (BK-2) recep
A;Reference number: JQ1488; MUID:92231936; PMID:1314587
A;Accession: JQ1488
A;Molecule type: mRNA
A;Residues: 1-364 <HES>
A;Cross-references: GB:M88714; NID:g1387999; PIDN:AAB02793.1; PID:g1388000
C;Genetics:
A;Gene: GDB:BDKRB2
A;Cross-references: GDB:135713; OMIM:113503
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A;Map position: 14q32.1-14q32.2
A;Introns: #status absent
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F;34-56/Domain: transmembrane #status predicted <TM1>
F;66-92/Domain: transmembrane #status predicted <TM2>
F;104-127/Domain: transmembrane #status predicted <TM3>
F;148-171/Domain: transmembrane #status predicted <TM4>
F;195-221/Domain: transmembrane #status predicted <TM5>
F;241-266/Domain: transmembrane #status predicted <TM6>
F;285-309/Domain: transmembrane #status predicted <TM7>
F;3,12,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;170,237,342/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status pre
F;242/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F;316/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

  Query Match            16.8%;  Score 350.5;  DB 2;  Length 364;
  Best Local Similarity  27.3%;  Pred. No. 1.2e-23;
  Matches  100;  Conservative   58;  Mismatches  141;  Indels   67;  Gaps    9;

Qy         29 VLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYV 88
Db         32 IQPPFLWVLFVLATLENIFVLSVFCLHKSSCTVAEIYLGNLAAADLILACGLPFWAITIS 91

Qy         89 RRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIIS 148
Db         92 NNFDWLFGETLCRVVNAIISMNLYSSICFLMLVSIDRYLALVKTMSMGRMRGVRWAKLYS 151

Qy        149 CLLWGITIGLTVHLL--KKKMPIQNGGANLCSSFSICHTFQW----HEAMFLLEFFLPLG 202
Db        152 LVIWGCTLLLSSPMLVFRTMKEYSDEGHNVTACVISYPSLIWEVFTNMLLNVVGFLLPLS 211

Qy        203 IILFCSARIIWSLRQRQMDRHAKI---KRAITFIMVVAIVFVICFLPSVVVRIRIFW-LL 258
Db        212 VITFCTMQIMQVLRNNEMQKFKEIQTERRATVLVLVVLLLFIICWLP---FQISTFLDTL 268

Qy        259 HTSG-TQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQRKM 317
Db        269 HRLGILSSCQDERIIDVITQIASFMAYSNSCLNPLVYVIVGKRF----------RKK 315

Qy        318 TGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGPTSNNHSKKGHCHQEPAS 377
Db        316 SWE---------------------------------VYQGV-----CQKGGCRSEPIQ 335

Qy        378 LEKQLG 383
Db        336 MENSMG 341


RESULT 7
JC5549
heptahelical P2Y5-like receptor - human
C;Species: Homo sapiens (man)
C;Date: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
C;Accession: JC5549
R;Janssens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.
Biochem. Biophys. Res. Commun. 236, 106-112, 1997
A;Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.
A;Reference number: JC5549; MUID:97366605; PMID:9223435
A;Accession: JC5549
A;Molecule type: DNA
A;Residues: 1-370 <JAN>
A;Cross-references: UNIPROT:Q99677; DDBJ:AF005419; NID:g2240034; PIDN:AAB66322.1; PID:g2
C;Superfamily: ATP receptor P2u

  Query Match            16.7%;  Score 348.5;  DB 2;  Length 370;
  Best Local Similarity  29.6%;  Pred. No. 1.9e-23;
  Matches   89;  Conservative   63;  Mismatches  130;  Indels   19;  Gaps    9;

Qy         17 NCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76
Db         29 NTCIVDDSFKYNLNGAVYSVVFILGLITNSVSLFVFCFRMKMRSETAIFITNLAVSDLLF 88

Qy         77 IICLPF-LMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHA 135
Db         89 VCTLPFKIFYNFNRH--WPFGDTLCKISGTAFLTNIYGSMLFLTCISVDRFLAIVYPFRS 146

Qy        136 LNKISNRTAAIISCLLWGITI--GLTVHLLKKKMPIQNGGANLC---SSFSICHTFQWHE 190
Db        147 RTIRTRRNSAIVCAGVWILVLSGGISASLFSTTN--VNNATTTCFEGLSKRVWKTYLSKI 204

Qy        191 AMFL--LEFFLPLGIILFCSARIIWSLRQ----RQMDRHAKIKRAITFIMVVAIVFVICF 244
Db        205 TIFIEVVGFIIPLILNVSCSSVVLRTLRKPATLSQIGTNK--KKVLKMITVHMAVFVVCF 262

Qy        245 LPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNF 304
Db        263 VPYNSV-LFLYALVRSQAITNCFLERFAKIMYPITLCLATLNCCFDPFIYYFTLESFQKS 321

Qy        305 F 305
Db        322 F 322


RESULT 8
I55450
G protein-coupled P2 receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I55450
R;Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.
J. Biol. Chem. 270, 26152-26158, 1995
A;Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor.
A;Reference number: I55450; MUID:96064682; PMID:7592819
A;Accession: I55450
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <RES>
A;Cross-references: UNIPROT:Q63371; GB:D63665; NID:g1066007; PIDN:BAA09816.1; PID:g10660
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor

  Query Match            16.7%;  Score 348;  DB 2;  Length 328;
  Best Local Similarity  31.5%;  Pred. No. 1.9e-23;
  Matches   94;  Conservative   49;  Mismatches  133;  Indels   22;  Gaps    8;

Qy         19 CVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLII 78
Db         18 CVYREDFKRLLLPPVYSVVLVVGLPLNVCVIAQICASRRTLTRSAVYTLNLALADLLYAC 77

Qy         79 CLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNK 138
Db         78 SLPLLIYNYARGDHWPFGDLACRLVRFLFYANLHGSILFLTCISFQRYLGICHPLAPWHK 137

Qy        139 ISNRTAAIISC-LLWGITIGLTVHLLKKKMPIQNG---GANLCSSFS--ICHT--FQWHE 190
Db        138 RGGRRAAWVVCGVVW---LVVTAQCLPTAVFAATGIQRNRTVCYDLSPPILSTRYLPYGM 194

Qy        191 AMFLLEFFLPLGIILFCSARIIWSLRQRQ-------MDRHAKIKRAITFIMVVAIVFVIC 243
Db        195 ALTVIGFLLPFTALLACYCRMARRLCRQDGPAGPVAQERRSKAAR---MAVVVAAVFVIS 251

Qy        244 FLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF 301
Db        252 FLPFHITKTAYLAVRSTPGV-SCPVLETFAAAYKGTRPFASANSVLDPILFYFTQQKF 308


RESULT 9
I48705
proteinase activated receptor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48705
R;Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J.
J. Biol. Chem. 270, 5950-5955, 1995
A;Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and f
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A;Reference number: I48705; MUID:95197620; PMID:7890726
A;Accession: I48705
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-399 <RES>
A;Cross-references: UNIPROT:P55086; EMBL:Z48043; NID:g663020; PIDN:CAA88097.1; PID:g663(
C;Superfamily: ATP receptor P2u

  Query Match           16.4%;  Score 341;  DB 2;  Length 399;
  Best Local Similarity   30.5%;  Pred. No. 9.8e-23;
  Matches   92;  Conservative   59;  Mismatches  127;  Indels   24;  Gaps    9;

Qy         13 IDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVA 72
              ||: :  :          || | . : |: ||  ||:||||| |  |    : |:: |||:|
Db         63 IDEFSASILTGKLTTVFLPVVYIIVFVIGLPSNGMALWIFLFRTKKKHPAVIYMANLALA 122

Qy         73 DFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHP 132
              | | :|  |  :  ::   :| :|:  |::::     |   ||:|:| ::| ||: :|:|
Db        123 DLLSVIWFPLKISYHLHGNNWVYGEALCKVLIGFFYGNMYCSILFMTCLSVQRYWVIVNP 182

Qy        133 HHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQWHEAM 192
                  | :|  |  :|  :| :   :|: |   |  |      |:    : ||      | :
Db        183 MGHPRKKAN-IAVGVSLAIWLLIFLVTIPLYVMKQTIYIPALNI----TTCHDVLPEEVL 237

Qy        193 F--LLEFFLPL--GIILF-----CSARI--IWSLRQRQMDRHA--KIKRAITFIMVVAIV 239
              :  :|| |  |: ||       || :  | :||  || |:  | :|||  |: |  :
Db        238 VGDMFNYFLSLAIGVFLFPALLTASAYVLMIKTLRSSAMDEHSEKKRQRAIRLIITVLAM 297

Qy        240 FVICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSP 299
              : ||| || :: :  ::|: |   :   ||      : : |  : :|| :|| |||| |
Db        298 YFICFAPSNLLLVVHYFLIKTQ--RQSHVY----ALYLVALCLSTLNSCIDPFVYYFVSK 351

Qy        300 SF 301
              . |
Db        352 DF 353


RESULT 10
T09508
intron 17 purinergic receptor P2Y5 - human
N;Alternate names: G-protein coupled receptor
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09508
R;Bohm, S.K.; Trumpp, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.
submitted to the EMBL Data Library, April 1997
A;Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinob
A;Reference number: Z16705
A;Accession: T09508
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-344 <BOH>
A;Cross-references: UNIPROT:P43657; EMBL:AF000546; NID:g2232068; PID:g2232069
C;Genetics:
A;Map position: 13
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

  Query Match           16.3%;  Score 339.5;  DB 2;  Length 344;
  Best Local Similarity   28.2%;  Pred. No. 1.1e-22;
  Matches   83;  Conservative   65;  Mismatches  135;  Indels   11;  Gaps    7;

Qy         19 CVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLII 78
              | : | |   :   :  : |: ||: | :|::||   ||    :  :: |||::| | :
Db          9 CFYNDSFKYTLYGCMFSMVFVLGLVSNCVAIYIFICVLKVRNETTTYMINLAMSDLLFVF 68

Qy         79 CLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNK 138
                 |||  :  :   | :| |||: |:: : :   |  |||:||| ::|||:  :|:|  :
Db         69 TLPFRIFYFTTR-NWPFGDLLCKISVMLFYTNMYGSILFLTCISVDRFLAIVYPFKSKTL 127

Qy        139 ISNRTAAIISCLLWGITIG--LTVHLLKKKMPIQNGGANLC-SSF--SICHTFQWHEAMF 193
              : | | |:   :|   ||       ::      |  :  |  :|  :   |:     :|
Db        128 RTKRNAKIVCTGVWLTVIGGSAPAVFVQSTHSQGNNASEACFENFPEATWKTYLSRIVIF 187

Qy        194 --LLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIK--RAITFIMVVAIVFVICFLPSVV 249
                  :: ||:|| : : ||: :: :| :      :||   : :  | |  |:|  ||:|
Db        188 IEIVGFFIPLILNVTCSSMVLKTLTKPVTLSRSKINKTKVLKMIFVHLIIFCFCFVP-YN 246

Qy        250 VRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPN 303
              : : :: |: |     || |  :|   : |||      |   ||:||||:| :  |
Db        247 INLILYSLVRTQTFVNCSVVAAVRTMYPITLCIAVSNCCFDPIVYYFTSDTIQN 300


RESULT 11
A47556
ATP receptor P2u - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: A47556
R;Lustig, K.D.; Shiau, A.K.; Brake, A.J.; Julius, D.
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993
A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.
A;Reference number: A47556; MUID:93281707; PMID:7685114
A;Accession: A47556
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <LUS>
A;Cross-references: UNIPROT:P35383; GB:L14751; NID:g309457; PIDN:AAA39871.1; PID:g309458
C;Superfamily: ATP receptor P2u
C;Keywords: transmembrane protein

  Query Match           16.2%;  Score 337;  DB 2;  Length 373;
  Best Local Similarity   27.5%;  Pred. No. 2.1e-22;
  Matches   97;  Conservative   56;  Mismatches  158;  Indels   42;  Gaps    6;

Qy         19 CVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLII 78
              | | :||   :||   |:  : ||  | :||:||   ||:| :|  ::|:|||:| |
Db         25 CRFNEDFKYVLLPVSYGVVCVLGLCLNVVALYIFLCRLKTWNASTTYMFHLAVSDSLYAA 84

Qy         79 CLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNK 138
               || |:  | |   | |  : |:|: |:   |  ||:||| ::| |   |: | |:|
Db         85 SLPLLVYYYARGDHWPFSTVLCKLVRFLFYTNLYCSILFLTCISVHRCLGVLRPLHSLRW 144

Qy        139 ISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSFS----ICHTFQWHEAMFL 194
              | |  :: ::| : :     :|          |    |    |      |   :   |
Db        145 GRARYARRVAAVVWVLVLACQAPVLYFVTTSVRGTRITCHDTSARELFSHFVAYSSVMLG 204

Qy        195 LEFFLPLGIILFCSARIIWSLRQRQMDR----------HAKIKRAITFIMVVAIVFVICF 244
              | | :|  :|| |      : |  |:: :           || |    |  :|:| || :||
Db        205 LLFAVPFSVILVC-----YVLMARRLLKPAYGTTGGLPRAKRKSVRTIALVLA-VFALCF 258

Qy        245 LPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNF 304
              ||  |   |  :    |  :|    ::::|: ||      || ||||:|: :      |
Db        259 LPFHVT--RTLYYSFRSLDLSCHTLNAINMAYKITRPLASANSCLDPVLYFLAGQRLVRF 316

Qy        305 FSTL-------------------INRCLQRKMTGEPDNNRSTSVELTGDPNK 337
                                     || ::: ::   |::| |     |   |
Db        317 ARDAKPPTEPTPSPQARRKLGLHRPNRTVRKDLSVSSDDSRRTESTPAGSETK 369


RESULT 12
S66518
proteinase-activated receptor 2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66518; S64709; G02131
R;Nystedt, S.; Emilsson, K.; Larsson, A.K.; Stroembeck, B.; Sundelin, J.
Eur. J. Biochem. 232, 84-89, 1995
A;Title: Molecular cloning and functional expression of the gene encoding the human prot
A;Reference number: S66518; MUID:96048032; PMID:7556175
A;Accession: S66518
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <NYS>
A;Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:g1008084; PIDN:CAA90290.1; PID:g100
R;Boehm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn
```

Biochem. J. 314, 1009-1016, 1996
A;Title: Molecular cloning, expression and potential functions of the human proteinase-a
A;Reference number: S64709; MUID:96177879; PMID:8615752
A;Accession: S64709
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137,'A',139-397 <BOE>
A;Cross-references: EMBL:U34038; NID:g1041728; PIDN:AAB47871.1; PID:g1041729
A;Note: the authors translated the codon GTC for residue 68 as Ile and AAC for residue 2
R;Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
A;Reference number: H00822
A;Accession: G02131
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 29-397 <KAH>
A;Cross-references: EMBL:U36753; NID:g1208539; PIDN:AAA90957.1; PID:g1208540
C;Genetics:
A;Map position: 5q13
A;Introns: 28/1
C;Superfamily: ATP receptor P2u
F;1-36/Domain: activation peptide #status predicted <APT>
F;1-25/Domain: signal sequence #status predicted <SIG>
F;37-397/Product: proteinase-activated receptor 2 #status predicted <MAT>

Query Match 16.2%; Score 337; DB 2; Length 397;
Best Local Similarity 26.2%; Pred. No. 2.2e-22;
Matches 100; Conservative 68; Mismatches 153; Indels 60; Gaps 9;

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Qy         13 IDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVA 72
Db         61 VDEFSASVLTGKLTTVFLPIVYTIVFVVGLPSNGMALWVFLFRTKKKHPAVIYMANLALA 120

Qy         73 DFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHP 132
Db        121 DLLSVIWFPLKIAYHIHGNNWIYGEALCNVLIGFFYGNMYCSILFMTCLSVQRYWVIVNP 180

Qy        133 HHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQWHEAM 192
Db        181 MGHSRKKAN-IAIGISLAIWLLILLVTIPLYVVKQTIFIPALNI----TTCHDVLPEQLL 235

Qy        193 F--LLEFFLPL--GIILF-----CSARI--IWSLRQRQMDRHA--KIKRAITFIMVVAIV 239
Db        236 VGDMFNYFLSLAIGVFLFPAFLTASAYVLMIRMLRSSAMDENSEKKRKRAIKLIVTVLAM 295

Qy        240 FVICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSP 299
Db        296 YLICFTPSNLLLVVHYFLIKSQGQSH------VYALYIVALCLSTLNSCIDPFVYYFVSH 349

Qy        300 SFPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLG 359
Db        350 DFRDH-----------------------------------AKNALLCRSVRTVKQMQVS 373

Qy        360 PTSNNHSKKGHCHQEPASLEK 380
Db        374 LTSKKHSRKSSSYSSSSTTVK 394
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RESULT 13
A40191
platelet-activating factor receptor - human
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
C;Accession: A40191; JH0479; A41079; JC1359; A42831; I51923
R;Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A;Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell sur
A;Reference number: A40191; MUID:92250505; PMID:1374385
A;Accession: A40191
A;Molecule type: mRNA
A;Residues: 1-342 <KUN>
A;Cross-references: UNIPROT:P25105; GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:g456294
R;Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G.
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A;Title: Characterization of a human cDNA that encodes a functional receptor for platelet
A;Reference number: JH0479; MUID:92028922; PMID:1656963
A;Accession: JH0479
A;Molecule type: mRNA
A;Residues: 1-342 <YER>
A;Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538
A;Experimental source: granulocyte, cell line HL-60 all
R;Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.; Minami, M.; Bito, H.; Seya
J. Biol. Chem. 266, 20400-20405, 1991
A;Title: Molecular cloning and expression of platelet-activating factor receptor from hum
A;Reference number: A41079; MUID:92041873; PMID:1657923
A;Accession: A41079
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-342 <NAK>
A;Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BAA01050.1; PID:g219976
R;Sugimoto, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y.
Biochem. Biophys. Res. Commun. 189, 617-624, 1992
A;Title: Molecular cloning and characterization of the platelet-activating factor recepto
A;Reference number: JC1359; MUID:93112021; PMID:1281995
A;Accession: JC1359
A;Molecule type: mRNA
A;Residues: 1-315,'N',317-342 <SUG>
A;Experimental source: heart
A;Note: the authors translated the codon AAT for residue 316 as Lys
R;Seyfried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.
Genomics 13, 832-834, 1992
A;Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns a
A;Reference number: A42831; MUID:92347886; PMID:1322356
A;Accession: A42831
A;Molecule type: DNA
A;Residues: 1-226,'TG',229-342 <SEY>
A;Cross-references: GB:M88177; NID:g190697; PIDN:AAA60214.1; PID:g190698
A;Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIP:109814)
R;Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993
A;Title: Cloning of a human platelet-activating factor receptor gene: evidence for an int
A;Reference number: I51923; MUID:93192035; PMID:8383507
A;Accession: I51923
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-342 <RES>
A;Cross-references: GB:S56396; NID:g298580; PIDN:AAB25755.1; PID:g298581
C;Genetics:
A;Gene: GDB:PTAFR
A;Cross-references: GDB:128806; OMIM:173393
A;Map position: 1p35-1p34.3
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein
F;17-38/Domain: transmembrane #status predicted <TRI>
F;54-75/Domain: transmembrane #status predicted <TII>
F;92-113/Domain: transmembrane #status predicted <III>
F;134-155/Domain: transmembrane #status predicted <TIV>
F;184-205/Domain: transmembrane #status predicted <TRV>
F;233-253/Domain: transmembrane #status predicted <TVI>
F;277-297/Domain: transmembrane #status predicted <VII>

Query Match 16.0%; Score 333; DB 2; Length 342;
Best Local Similarity 27.9%; Pred. No. 4.3e-22;
Matches 89; Conservative 58; Mismatches 140; Indels 32; Gaps 8;

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Qy         24 DFIVKVLPPVLGLEFIFGLLGNGLALWIFC--FHLKSWKSSRIFLFNLAVADFLLIICLP 81
Db         12 EFRYTLFPIVYSIIFVLGVIANGYVLWVFARLYPCKKFNEIKIFMVNLTMADMLFLITLP 71

Qy         82 FLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISN 141
Db         72 LWIVYYQNQGNWILPKFLCNVAGCLFFINTYCSVAFLGVITYNRFQAVTRPIKTAQANTR 131

Qy        142 RTAAIISCLLWGITIGLTVHLL----KKKMPIQNGGANLCSSFS----------ICHTFQ 187
Db        132 KRGISLSLVIWVAIVGAASYFLILDSTNTVPDSAGSGNVTRCFEHYEKGSVPVLIIHIF- 190
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Qy        188 WHEAMFLLEFFLPLGIILFCSARIIWSLRQR--QMDRHAKIK-RAITFIMVVAIVFVICF 244
Db        191 -----IVFSFFLVFLIILFCNLVIIRTLLMQPVQQQRNAEVKRRALWMVCTVLAVFIICF 245

Qy        245 LPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF--- 301
Db        246 VPHHVVQLP--WTLAELGFQDSKFHQAINDAHQVTLCLLSTNCVLDPVIYCFLTKKFRKH 303

Qy        302 --PNFFSTLINRCLQRKMT 318
Db        304 LTEKFYSMRSSRKCSRATT 322
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RESULT 14
A47249
brain-specific somatostatin receptor SSTR-4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47249
R;Bruno, J.F.; Xu, Y.; Song, J.; Berelowitz, M.
Proc. Natl. Acad. Sci. U.S.A. 89, 11151-11155, 1992
A;Title: Molecular cloning and functional expression of a brain-specific somatostatin re
A;Reference number: A47249; MUID:93087484; PMID:1360663
A;Accession: A47249
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-384 <BRU>
A;Cross-references: UNIPROT:P30937; GB:M96544; NID:g207072; PIDN:AAA42180.1; PID:g207073
A;Note: sequence extracted from NCBI backbone (NCBIN:119731, NCBIP:119732)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 15.9%; Score 330.5; DB 2; Length 384;
Best Local Similarity 27.7%; Pred. No. 8.1e-22;
Matches 102; Conservative 58; Mismatches 141; Indels 67; Gaps 12;

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Qy         33 VLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRWD 92
Db         49 IYALVCLVGLVGNALVIFVILRYAKMKTATNIYLLNLAVADELFMLSVPFVASAAALR-H 107

Qy         93 WKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLW 152
Db        108 WPFGAVLCRAVLSVDGLNMFTSVFCLTVLSVDRYVAVVHPLRAATYRRPSVAKLINLGVW 167

Qy        153 --GITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQW-HEA-------MFLLEFFLPL 201
Db        168 LASLLVTLPIAVFADTRPARGGEAVACN-------LHWPHPAWSAVFVIYTFLLGFLLPV 220

Qy        202 GIILFCSARIIW-----SLRQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFW 256
Db        221 LAIGLCYLLIVGKMRAVALRAGWQQRRRSEKKITRLVLMVVTVFVLCWMPFYVVQLLNLF 280

Qy        257 LLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFS-TLINRCLQR 315
Db        281 VTSLDATVN----------HVSLILSYANSCANPILYGFLSDNFRRSFQRVLCLRCCLL 329

Qy        316 KMTG---EPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGPTSNNHSKKGHC 371
Db        330 ETTGGAEEEPLDYYATAL-------KSRGGPGCIC-----PPLP--------------C 362

Qy        372 HQEPASLE 379
Db        363 QQEPMQAE 370
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RESULT 15
OORTB2
bradykinin receptor type B-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A41283; A55079; S47529
R;McEachern, A.E.; Shelton, E.R.; Bhakta, S.; Obernolte, R.; Bach, C.; Zuppan, P.; Fujis
Proc. Natl. Acad. Sci. U.S.A. 88, 7724-7728, 1991
A;Title: Expression cloning of a rat B-2 bradykinin receptor.
A;Reference number: A41283; MUID:91352062; PMID:1715575
A;Accession: A41283
A;Molecule type: mRNA
A;Residues: 1-366 <MCE>
A;Cross-references: UNIPROT:P25023; GB:M59967
R;Pesquero, J.B.; Lindsey, C.J.; Zeh, K.; Paiva, A.C.M.; Ganten, D.; Bader, M.
J. Biol. Chem. 269, 26920-26925, 1994
A;Title: Molecular structure and expression of rat bradykinin B2 receptor gene. Evidence
A;Reference number: A55079; MUID:95014558; PMID:7929432
A;Accession: A55079
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-75,'A',77-366 <PES>
A;Cross-references: GB:X80187; GB:X80188; GB:X80189; GB:X80190
R;Wang, D.; Ma, J.; Chao, L.; Chao, J.
Biochim. Biophys. Acta 1219, 171-174, 1994
A;Title: Molecular cloning and sequence analysis of rat bradykinin B(2) receptor gene.
A;Reference number: S47529; MUID:94368850; PMID:8086459
A;Accession: S47529
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-366 <WAN>
A;Cross-references: EMBL:L26173; NID:g476749; PIDN:AAA62492.1; PID:g685244
C;Comment: This G protein-coupled receptor binds the nonapeptide bradykinin.
C;Superfamily: vertebrate rhodopsin
C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; lipoprotein;
F;31-48/Domain: transmembrane #status predicted <TM1>
F;79-96/Domain: transmembrane #status predicted <TM2>
F;107-126/Domain: transmembrane #status predicted <TM3> .
F;154-170/Domain: transmembrane #status predicted <TM4>
F;197-215/Domain: transmembrane #status predicted <TM5>
F;245-261/Domain: transmembrane #status predicted <TM6>
F;3,14,182/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;105-186/Disulfide bonds: #status predicted
F;326/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 15.7%; Score 326.5; DB 1; Length 366;
Best Local Similarity 26.7%; Pred. No. 1.8e-21;
Matches 97; Conservative 56; Mismatches 143; Indels 67; Gaps 8;

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Qy         32 PVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRW 91
Db         37 PFLWVLFLLAALENIFVLSVFCLHKTNCTVAEIYLGNLAGADLILACGLPFWAITIANNF 96

Qy         92 DWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLL 151
Db         97 DWLFGEVLCRVVNTMIYMNLYSSICFLMLVSIDRYLALVKTMSMGRMRGVRWAKLYSLVI 156

Qy        152 WGITIGLTVHLL--KKKMPIQNGGANLCSSFSICHTFQW----HEAMFLLEFFLPLGIIL 205
Db        157 WSCTLLLSSPMLVFRTMKDYREEGHNVTACVIVYPSRSWEVFTNMLLNLVGFLLPLSIIT 216

Qy        206 FCSARIIWSLRQRQMDRHAKI---KRAITFIMVVAIVFVICFLPSVVVRIRIF--WLLHT 260
Db        217 FCTVRIMQVLRNNEMKKFKEVQTEKKATVLVLAVLGLFVLCWFP---FQISTFLDTLLRL 273

Qy        261 SGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQRKMTGE 320
Db        274 GVLSGCWNERAVDIVTQISSYVAYSNSCLNPLVYVIVGKRF-------------RK---- 316

Qy        321 PDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGPTSNNHSKKGHCHQEPASLEK 380
Db        317 ----------------KSREVYQAI-------------------CRKGGCMGESVQMEN 340

Qy        381 QLG 383
Db        341 SMG 343
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Search completed: October 20, 2005, 06:04:42
Job time : 18 secs

OM protein - protein search, using sw model

Run on: October 20, 2005, 05:58:30 ; Search time 59 Seconds
(without alignments)
3358.892 Million cell updates/sec

Title: US-10-800-249-2
Perfect score: 2081
Sequence: 1 MNRHHLQDHFLEIDKKNCCV.....KGHCHQEPASLEKQLGCCIE 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1995	95.9	387	2	Q8NGE4	Q8nge4 homo sapien
2	1990	95.6	387	1	G09B_HUMAN	P49019 homo sapien
3	1935	93.0	363	2	Q8TDS4	Q8tds4 homo sapien
4	1591	76.5	360	2	Q80Z39	Q80z39 rattus norv
5	1577	75.8	360	2	Q9EP66	Q9ep66 mus musculu
6	1111	53.4	263	2	Q8NGV8	Q8ngv8 homo sapien
7	900.5	43.3	343	1	GP81_MOUSE	Q8c131 mus musculu
8	883.5	42.5	346	1	GP81_HUMAN	Q9bxc0 homo sapien
9	876.5	42.1	346	2	Q6NXU5	Q6nxu5 homo sapien
10	563	27.1	384	2	Q8NGW4	Q8ngw4 homo sapien
11	563	27.1	384	2	Q86WP7	Q86wp7 homo sapien
12	563	27.1	423	2	Q8TDS5	Q8tds5 homo sapien
13	496.5	23.9	319	2	Q9NQ20	Q9nq20 homo sapien
14	494.5	23.8	319	1	GP31_HUMAN	O00270 homo sapien
15	481	23.1	319	2	Q9JLS1	Q9jls1 mus musculu
16	431	20.7	362	1	P2YR_CHICK	P34996 gallus gall
17	431	20.7	362	1	P2YR_MELGA	P49652 meleagris g
18	420	20.2	373	1	P2YR_RAT	P49651 rattus norv
19	415.5	20.0	347	2	Q7ZZA4	Q7zza4 brachydanio
20	415	19.9	361	2	Q90X57	Q90x57 xenopus lae
21	415	19.9	373	1	P2YR_BOVIN	P48042 bos taurus
22	413.5	19.9	357	2	Q9DE05	Q9de05 raja erinac
23	410	19.7	373	1	P2YR_MOUSE	P49650 mus musculu
24	407	19.6	373	1	P2YR_HUMAN	P47900 homo sapien
25	407	19.6	373	2	Q8BMJ5	Q8bmj5 mus musculu
26	406	19.5	373	1	P2YR_CAVPO	P59902 cavia porce
27	386.5	18.6	349	2	Q6P852	Q6p852 xenopus tro
28	378.5	18.2	309	1	GP35_HUMAN	Q9hc97 homo sapien
29	376.5	18.1	394	2	Q6ZMP9	Q6zmp9 homo sapien
30	374.5	18.0	346	1	CLT2_HUMAN	Q9ns75 homo sapien
31	374	18.0	339	2	Q6NS65	Q6ns65 mus musculu
32	368	17.7	374	2	O57466	O57466 meleagris g
33	358	17.2	309	1	CLT2_RAT	Q924t9 rattus norv
34	358	17.2	537	1	P2Y8_XENLA	P79928 xenopus lae
35	358	17.2	537	2	Q7ZWQ7	Q7zwq7 xenopus lae
36	354.5	17.0	370	2	Q6NSP5	Q6nsp5 homo sapien
37	353.5	17.0	370	1	P2Y9_HUMAN	Q99677 homo sapien
38	352.5	16.9	345	1	CLT2_PIG	Q95n03 sus scrofa
39	351.5	16.9	308	1	P2Y5_CHICK	P32250 gallus gall
40	350.5	16.8	307	2	Q8BS98	Q8bs98 mus musculu
41	350.5	16.8	364	2	Q68DM8	Q68dm8 homo sapien
42	350.5	16.8	391	1	BRB2_HUMAN	P30411 homo sapien
43	350	16.8	367	1	GP17_HUMAN	Q13304 homo sapien
44	349	16.8	361	1	P2Y4_MOUSE	Q9jjs7 mus musculu
45	348.5	16.7	370	2	Q8BKK1	Q8bkk1 mus musculu

ALIGNMENTS

RESULT 1
Q8NGE4
ID Q8NGE4 PRELIMINARY; PRT; 387 AA.
AC Q8NGE4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Seven transmembrane helix receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB065865; BAC06083.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR002286; P2_purnocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PRINTS; PR01157; P2YPURNOCPTR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 387 AA; 44495 MW; 26433C855E85EC81 CRC64;

Query Match 95.9%; Score 1995; DB 2; Length 387;
Best Local Similarity 96.1%; Pred. No. 7.1e-130;
Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

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Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| |||||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| ||||||||||||:||||||||:|||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
```

```
Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 2
G09B_HUMAN
ID   G09B_HUMAN     STANDARD;      PRT;   387 AA.
AC   P49019;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable G protein-coupled receptor GPR109B (G protein-coupled
DE   receptor HM74).
GN   Name=GPR109B; Synonyms=HM74;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Monocytes;
RX   MEDLINE=94092629; PubMed=7505609;
RA   Nomura H., Nielsen B.W., Matsushima K.;
RT   "Molecular cloning of cDNAs encoding a LD78 receptor and putative
RT   leukocyte chemotactic peptide receptors.";
RL   Int. Immunol. 5:1239-1249(1993).
CC   -!- FUNCTION: Orphan receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10923; BAA01721.1; -.
DR   PIR; I69202; I69202.
DR   HSSP; P34996; 1DDD.
DR   Genew; HGNC:16824; GPR109B.
DR   MIM; 606039; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane.
FT   DOMAIN        1     28       Extracellular (Potential).
FT   TRANSMEM     29     50       1 (Potential).
FT   DOMAIN       51     63       Cytoplasmic (Potential).
FT   TRANSMEM     64     85       2 (Potential).
FT   DOMAIN       86    102       Extracellular (Potential).
FT   TRANSMEM    103    123       3 (Potential).
FT   DOMAIN      124    142       Cytoplasmic (Potential).
FT   TRANSMEM    143    163       4 (Potential).
FT   DOMAIN      164    194       Extracellular (Potential).
FT   TRANSMEM    195    209       5 (Potential).
FT   DOMAIN      210    236       Cytoplasmic (Potential).
FT   TRANSMEM    237    256       6 (Potential).
FT   DOMAIN      257    273       Extracellular (Potential).
FT   TRANSMEM    274    298       7 (Potential).
FT   DOMAIN      299    387       Cytoplasmic (Potential).
FT   DISULFID    100    177       By similarity.
SQ   SEQUENCE   387 AA;  44481 MW;  C244F562C2343647 CRC64;

  Query Match             95.6%;  Score 1990;  DB 1;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 1.6e-129;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| || |||||||:||| ||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 3
Q8TDS4
ID   Q8TDS4      PRELIMINARY;      PRT;   363 AA.
AC   Q8TDS4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein-coupled receptor HM74a (Seven transmembrane helix
DE   receptor).
GN   Name=GPCR;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22513958; PubMed=12522134; DOI=10.1074/jbc.M210695200;
RA   Wise A., Foord S.M., Fraser N.J., Barnes A.A., Elshourbagy N.,
RA   Eilert M., Ignar D.M., Murdock P.R., Steplewski K., Green A.,
RA   Brown A.J., Dowell S.J., Szekeres P.G., Hassall D.G., Marshall F.H.,
RA   Wilson S., Pike N.B.;
RT   "Molecular identification of high and low affinity receptors for
RT   nicotinic acid.";
RL   J. Biol. Chem. 278:9869-9874(2003).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Elshourbagy N.A.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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RN   [4]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB083632; BAB89345.1; -.
DR   EMBL; AY148884; AAN71621.1; -.
DR   EMBL; AB065876; BAC06094.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01157; P2YPURNOCPTR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   363 AA;  41849 MW;  C4B0EEC9CCB81D56 CRC64;

  Query Match             93.0%;  Score 1935;  DB 2;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-126;
  Matches  362;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TS 362
              ||
Db        361 TS 362


RESULT 4
Q80Z39
ID   Q80Z39      PRELIMINARY;      PRT;   360 AA.
AC   Q80Z39;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Nicotinic acid receptor.
GN   Name=HM74b;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Soga T., Kamhara M., Takasaki J., Matsumoto S., Saito T., Ohishi T.,
RA   Hiyama H., Matsuo A., Matsushime H., Furuichi K.;
RT   "Molecular identification of nicotinic acid receptor.";
RL   Biochem. Biophys. Res. Commun. 0:0-0(2003).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB103062; BAC58009.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   360 AA;  41458 MW;  975BDEBCA448A6C5 CRC64;

  Query Match             76.5%;  Score 1591;  DB 2;  Length 360;
  Best Local Similarity   83.7%;  Pred. No. 5e-102;
  Matches  298;  Conservative   18;  Mismatches   40;  Indels    0;  Gaps    0;

Qy          7 QDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFL 66
              |:||| |: |||||||: | ||||||||||:||||||||||||||||||||||||||||
Db          4 QNHFLVINGKNCCVFRDENIAKVLPPVLGLEFVFGLLGNGLALWIFCFHLKSWKSSRIFL 63

Qy         67 FNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRY 126
              |||||||||||||||| ||||: |||:|| ||||:||||||||||||||||||||||||
Db         64 FNLAVADFLLIICLPFLTDNYVQNWDWRFGSIPCRVMLFMLAMNRQGSIIFLTVVAVDRY 123

Qy        127 FRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSFSICHTF 186
              |||||||| |||||||||||||| ||||||||||||   |  :|| ||||||||||:||
Db        124 FRVVHPHHFLNKISNRTAAIISCFLWGITIGLTVHLLYTDMMTRNGDANLCSSFSICYTF 183

Qy        187 QWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICFLP 246
              :||:|||||||||||||||| |||||||||||||| |||||| ||||||||||||||||
Db        184 RWHDAMFLLEFFLPLGIILFCSGRIIWSLRQRQMDRHVKIKRAINFIMVVAIVFVICFLP 243

Qy        247 SVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFS 306
              || |||||||||:    :||::| ||||||| ||||||||||||||||||||||||||||
Db        244 SVAVRIRIFWLLYKHNVRNCDIYSSVDLAFFTTLSFTYMNSMLDPVVYYFSSPSFPNFFS 303

Qy        307 TLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGPTS 362
              | |||||:||  ||||||||||||||||:  |  | ||| :  || || ||  ||
Db        304 TCINRCLRRKTLGEPDNNRSTSVELTGDPSTIRSIPGALMTDPSEPGSPPYLASTS 359


RESULT 5
Q9EP66
ID   Q9EP66      PRELIMINARY;      PRT;   360 AA.
AC   Q9EP66;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative seven transmembrane spanning receptor.
GN   Name=Gpr109b; Synonyms=Puma-g, Pumag;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SvJ, and C57BL/6;
RA   Schaub A., Futterer A., Pfeffer K.;
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AJ300199; CAC17791.1; -.
DR   EMBL; AJ300198; CAC17790.1; -.
DR   MGD; MGI:1933383; Gpr109b.
DR   GO; GO:0016021; C:integral to membrane; IDA.
DR   GO; GO:0005525; F:GTP binding; IDA.
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DR   GO; GO:0001614; F:purinergic nucleotide receptor activity; IDA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   360 AA;  41400 MW;  CCCE52A2475777FC CRC64;

  Query Match             75.8%;  Score 1577;  DB 2;  Length 360;
  Best Local Similarity   83.1%;  Pred. No. 4.7e-101;
  Matches  295;  Conservative   19;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          8 DHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLF 67
              |||| |: |||||||: | ||||||||||:|||||||||||||||||||||||||||||
Db          5 DHFLVINGKNCCVFRDENIAKVLPPVLGLEFVFGLLGNGLALWIFCFHLKSWKSSRIFLF 64

Qy         68 NLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYF 127
              |||||||||||||||| ||||  |||:|| ||||:|||||||||||||||||||||||||
Db         65 NLAVADFLLIICLPFLTDNYVHNWDWRFGGIPCRVMLFMLAMNRQGSIIFLTVVAVDRYF 124

Qy        128 RVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQ 187
              ||||||| |||||||||||||| |||:|||||||||    |  :|| | ||||||||: |:
Db        125 RVVHPHHFLNKISNRTAAIISCFLWGLTIGLTVHLLYTNMMTKNGEAYLCSSFSICYNFR 184

Qy        188 WHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICFLPS 247
              ||:|||||||||||| |||||| |||||||||||||||||||| |||||||||:||||||
Db        185 WHDAMFLLEFFLPLAIILFCSGRIIWSLRQRQMDRHAKIKRAINFIMVVAIVFIICFLPS 244

Qy        248 VVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFST 307
              | |||||||||:    :||::| ||||||| ||||||||||||||||||||||||||||
Db        245 VAVRIRIFWLLYKYNVRNCDIYSSVDLAFFTTLSFTYMNSMLDPVVYYFSSPSFPNFFST 304

Qy        308 LINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGPTS 362
               |||||::|  |||||||||||||||||: ||  | ||||:  || || ||  ||
Db        305 CINRCLRKKTLGEPDNNRSTSVELTGDPSTTRSIPGALMADPSEPGSPPYLASTS 359


RESULT 6
Q8NGV8
ID   Q8NGV8      PRELIMINARY;      PRT;   263 AA.
AC   Q8NGV8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Seven transmembrane helix receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB065665; BAC05891.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01157; P2YPURNOCPTR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   263 AA;  30289 MW;  F96BF023A5E1F1C1 CRC64;

  Query Match             53.4%;  Score 1111;  DB 2;  Length 263;
  Best Local Similarity   98.6%;  Pred. No. 5e-69;
  Matches  205;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||||||||||||||||||||||||||||||||| :|||||||||
Db        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIPDGGANLCSSF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCS 208
              ||||| ||||||||||||||||||||||
Db        181 SICHTLQWHEAMFLLEFFLPLGIILFCS 208


RESULT 7
GP81_MOUSE
ID   GP81_MOUSE     STANDARD;      PRT;   343 AA.
AC   Q8C131;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable G protein-coupled receptor GPR81.
GN   Name=Gpr81;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Skin;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
CC   -!- FUNCTION: Orphan receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AK029064; BAC26273.1; -.
DR   MGD; MGI:2441671; Gpr81.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR002286; P2_purnocptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN        1     21       Extracellular (Potential).
FT   TRANSMEM     22     42       1 (Potential).
FT   DOMAIN       43     49       Cytoplasmic (Potential).
FT   TRANSMEM     50     70       2 (Potential).
FT   DOMAIN       71     90       Extracellular (Potential).
FT   TRANSMEM     91    111       3 (Potential).
FT   DOMAIN      112    131       Cytoplasmic (Potential).
FT   TRANSMEM    132    152       4 (Potential).
FT   DOMAIN      153    182       Extracellular (Potential).
FT   TRANSMEM    183    203       5 (Potential).
FT   DOMAIN      204    220       Cytoplasmic (Potential).
FT   TRANSMEM    221    241       6 (Potential).
FT   DOMAIN      242    259       Extracellular (Potential).
FT   TRANSMEM    260    280       7 (Potential).
FT   DOMAIN      281    343       Cytoplasmic (Potential).
FT   DISULFID     88    165       By similarity.
FT   CARBOHYD      3      3       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   343 AA;  38927 MW;  917FA9499B2E03FD CRC64;

  Query Match           43.3%;  Score 900.5;  DB 1;  Length 343;
  Best Local Similarity  52.9%;  Pred. No. 2.2e-54;
  Matches  182;  Conservative   53;  Mismatches  100;  Indels    9;  Gaps    5;

Qy         13 IDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVA 72
              :|  :||:   : | :|:||:| | |: | ||||:||  ||||:|:|||| |:|||||||
Db          1 MDNGSCCLIEGEPISQVMPPLLILVFVLGALGNGIALCGFCFHMKTWKSSTIYLFNLAVA 60

Qy         73 DFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHP 132
              ||||:||||   | |:||  | |||| |||:|| ||||| |||:||||||||||:||||
Db         61 DFLLMICLPLRTDYYLRRRHWIFGDIACRLVLFKLAMNRAGSIVFLTVVAVDRYFKVVHP 120

Qy        133 HHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQWHEAM 192
              || :| ||||||| :|:|| : |  ||:|| :      |  : | || :     ||: |
Db        121 HHMVNAISNRTAAATACVLWTLVILGTVYLLMESHLCVQGTLSSCESFIMESANGWHDVM 180

Qy        193 FLLEFFLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVR 251
              | ||||||| |||||  ::||||:| |: | |:::||  |||||| ||: |:||||: |
Db        181 FQLEFFLPLTIILFCSVNVVWSLRRRQQLTRQARMRRATRFIMVVASVFITCYLPSVLAR 240

Qy        252 IRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINR 311
              :   | : ||    |:   ||  |  :||||||:||||||:||||||| | |:: |
Db        241 LYFLWTVPTSA---CD--PSVHTALHVTLSFTYLNSMLDPLVYYFSSPSLPKFYTKLTIC 295

Qy        312 CLQRKMTGEPDNNRSTSVELTGDPNKTR--GAPEALMANSGEPW 353
               |: |  |      ||  : ::   :|:   ||  :   : |: |
Db        296 SLKPKRPGRTKTRRSEEMPISNLCSKSSIDGANRSQRPSDGQ-W 338


RESULT 8
GP81_HUMAN
ID   GP81_HUMAN     STANDARD;      PRT;   346 AA.
AC   Q9BXC0;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable G protein-coupled receptor GPR81 (FKSG80 protein).
GN   Name=GPR81; Synonyms=FKSG80;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RX   MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
RA   Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
RA   Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT   "Discovery and mapping of ten novel G protein-coupled receptor
RT   genes.";
RL   Gene 275:83-91(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT   "Identification of G protein-coupled receptor genes from the human
RT   genome sequence.";
RL   FEBS Lett. 520:97-101(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Wang Y.-G., Gong L.;
RT   "Molecular cloning of FKSG80, a novel gene encoding a putative
RT   chemokine receptor.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT   "Genome-wide discovery and analysis of human seven transmembrane helix
RT   receptor genes.";
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Orphan receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in pituitary tissue. Not detected in
CC       frontal, temporal and occipital lobes of the cortex, basal
CC       forebrain, caudate nucleus, nucleus accumbens, and hippocampus.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF411110; AAL26481.1; -.
DR   EMBL; AB083631; BAB89344.1; -.
DR   EMBL; AF345568; AAK29071.1; -.
DR   EMBL; AB065866; BAC06084.1; -.
DR   Genew; HGNC:4532; GPR81.
DR   MIM; 606923; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Transmembrane.
FT   DOMAIN        1     21       Extracellular (Potential).
FT   TRANSMEM     22     42       1 (Potential).
FT   DOMAIN       43     49       Cytoplasmic (Potential).
FT   TRANSMEM     50     70       2 (Potential).
FT   DOMAIN       71     89       Extracellular (Potential).
FT   TRANSMEM     90    110       3 (Potential).
FT   DOMAIN      111    130       Cytoplasmic (Potential).
FT   TRANSMEM    131    151       4 (Potential).
FT   DOMAIN      152    182       Extracellular (Potential).
FT   TRANSMEM    183    203       5 (Potential).
FT   DOMAIN      204    220       Cytoplasmic (Potential).
FT   TRANSMEM    221    241       6 (Potential).
FT   DOMAIN      242    261       Extracellular (Potential).
FT   TRANSMEM    262    281       7 (Potential).
FT   DOMAIN      282    346       Cytoplasmic (Potential).
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FT   DISULFID     88    165       By similarity.
FT   CARBOHYD      3      3       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   346 AA;  39295 MW;  E0DB114EEB3A47A5 CRC64;

  Query Match             42.5%;  Score 883.5;  DB 1;  Length 346;
  Best Local Similarity   52.8%;  Pred. No. 3.2e-53;
  Matches  180;  Conservative   47;  Mismatches  107;  Indels    7;  Gaps    4;

Qy         17 NCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76
              :||     | | :|:||:| : |: | ||||:||  ||||:|:|| | ::||||||||||
Db          5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64

Qy         77 IICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136
              :|||||  | |:||  | |||||||: || |||||| |||:|||||| ||||:|||||||:
Db         65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADRYFKVVHPHHAV 124

Qy        137 NKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQWHEAMFLLE 196
              | || | || | | || : |  ||:|| :       | | || :      ||: || ||
Db        125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184

Qy        197 FFLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIF 255
              ||:||||||||| :|:||||:| |: | |::|:|  |||||||||: |:||||  |:
Db        185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLYFL 244

Qy        256 WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315
              | : :|    |:   ||  |  ||||||||||||||:|||||||||| |:: |     |:
Db        245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299

Qy        316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
              | |     |   : ::    ::      :  : |   | |
Db        300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340


RESULT 9
Q6NXU5
ID   Q6NXU5      PRELIMINARY;      PRT;   346 AA.
AC   Q6NXU5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein-coupled receptor 81.
GN   Name=GPR81;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PCR rescued clones;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC066883; AAH66883.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   346 AA;  39209 MW;  F916A8C273E53E63 CRC64;

  Query Match             42.1%;  Score 876.5;  DB 2;  Length 346;
  Best Local Similarity   52.2%;  Pred. No. 9.9e-53;
  Matches  178;  Conservative   48;  Mismatches  108;  Indels    7;  Gaps    4;

Qy         17 NCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLL 76
              :||     | | :|:||:| : |: | ||||:||  ||||:|:|| | ::||||||||||
Db          5 SCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCFHMKTWKPSTVYLFNLAVADFLL 64

Qy         77 IICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHAL 136
              :|||||  | |:||  | |||||||: || |||||| |||:|||||| ||||:|||||||:
Db         65 MICLPFRTDYYLRRRHWAFGDIPCRVGLFTLAMNRAGSIVFLTVVAADKYFKAVHPHHAV 124

Qy        137 NKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQWHEAMFLLE 196
              | || | || | | || : |  ||:|| :       | | || :      ||: || ||
Db        125 NTISTRVAAGIVCTLWALVILGTVYLLLENHLCVQETAVSCESFIMESANGWHDIMFQLE 184

Qy        197 FFLPLGIILFCSARIIWSLRQR-QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIF 255
              ||:||||||||| :|:||||:| |: | |::|:|  |||||||||: |:||||  |:
Db        185 FFMPLGIILFCSFKIVWSLRRRQQLARQARMKKAARFIMVVAIVFITCYLPSVSARLYFL 244

Qy        256 WLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQR 315
              | : :|    |:   ||  |  ||||||||||||||:|||||||||| |:: |     |:
Db        245 WTVPSSA---CD--PSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKLKICSLKP 299

Qy        316 KMTGEPDNNRSTSVELTGDPNKT-RGAPEALMANSGEPWSP 355
              | |     |   : ::    ::      :  : |   | |
Db        300 KQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDP 340


RESULT 10
Q8NGW4
ID   Q8NGW4      PRELIMINARY;      PRT;   384 AA.
AC   Q8NGW4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Seven transmembrane helix receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA   Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB065652; BAC05878.1; -.
DR   GO; GO:0050648; F:5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; ISS.
DR   GO; GO:0050647; F:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; ISS.
DR   GO; GO:0050646; F:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; ISS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; ISS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; ISS.
DR   GO; GO:0030817; P:regulation of cAMP biosynthesis; ISS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
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DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   384 AA;  41426 MW;  1C8455FED8085F36 CRC64;

  Query Match             27.1%;  Score 563;  DB 2;  Length 384;
  Best Local Similarity   41.8%;  Pred. No. 4.7e-31;
  Matches  118;  Conservative   52;  Mismatches   88;  Indels   24;  Gaps    5;

Qy         30 LPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVR 89
              | |:| |||: ||:|| |||:||| | : | |: :|| :|  |||||  ||  :| |:
Db         56 LAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFLLISNLPLRVDYYLL 115

Qy         90 RWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISC 149
                 |:||   |:: |||| |: ||  |::||| :|::|| :|| ||| |:: |   || ::
Db        116 HETWRFGAAACKVNLFMLSTNRTASVVFLTAIALNRYLKVVQPHHVLSRASVGAAARVAG 175

Qy        150 LLWGITIGLTVHLLKKKMPIQNGGANLCSSFSI----CHTFQWHEAMFLLEFFLPLGIIL 205
               ||   : |  |||     :       | |: :      : :||:|::|||||||| :||
Db        176 GLWVGILLLNGHLL-----LSTFSGPSCLSYRVGTKPSASLRWHQALYLLEFFLPLALIL 230

Qy        206 FCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVV---VRIRIFWLLHTSG 262
              |    |  ::| | :   |  :||:  : :|  |: ||||||::     :  |||
Db        231 FAIVSIGLTIRNRGLGGQAGPQRAMRVLAMVVAVYTICFLPSIIFGMASMVAFWL----- 285

Qy        263 TQNCEVYRSVDLA---FFITLSFTYMNSMLDPVVYYFSSPSF 301
                  ||:||    |  :|:|||:||:||||:| ||||:|
Db        286 ----SACRSLDLCTQLFHGSLAFTYLNSVLDPVLYCFSSPNF 323


RESULT 11
Q86WP7
ID   Q86WP7      PRELIMINARY;      PRT;   384 AA.
AC   Q86WP7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative 5-oxo-ETE G-protein coupled receptor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22495202; PubMed=12606753;
RA   Jones C.E., Holden S., Tenaillon L., Bhatia U., Seuwen K., Tranter P.,
RA   Turner J., Kettle R., Bouhelal R., Charlton S., Nirmala N., Jarai G.,
RA   Finan P.;
RT   "Expression and characterization of a 5-oxo-6E,8Z,11Z,14Z-
RT   eicosatetraenoic acid receptor highly expressed on human eosinophils
RT   and neutrophils.";
RL   Mol. Pharmacol. 63:471-477(2003).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AY158687; AAO17739.1; -.
DR   GO; GO:0050648; F:5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; ISS.
DR   GO; GO:0050647; F:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; ISS.
DR   GO; GO:0050646; F:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; ISS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; ISS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; ISS.
DR   GO; GO:0030817; P:regulation of cAMP biosynthesis; ISS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   384 AA;  41412 MW;  0C5E35FED8085F36 CRC64;

  Query Match             27.1%;  Score 563;  DB 2;  Length 384;
  Best Local Similarity   41.8%;  Pred. No. 4.7e-31;
  Matches  118;  Conservative   52;  Mismatches   88;  Indels   24;  Gaps    5;

Qy         30 LPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVR 89
              | |:| |||: ||:|| |||:||| | : | |: :|| :|  |||||  ||  :| |:
Db         56 LAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFLLISNLPLRVDYYLL 115

Qy         90 RWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISC 149
                 |:||   |:: |||| |: ||  |::||| :|::|| :|| ||| |:: |   || ::
Db        116 HETWRFGAAACKVNLFMLSTNRTASVVFLTAIALNRYLKVVQPHHVLSRASVGAAARVAG 175

Qy        150 LLWGITIGLTVHLLKKKMPIQNGGANLCSSFSI----CHTFQWHEAMFLLEFFLPLGIIL 205
               ||   : |  |||     :       | |: :      : :||:|::|||||||| :||
Db        176 GLWVGILLLNGHLL-----LSTFSGPSCLSYRVGTKPSASLRWHQALYLLEFFLPLALIL 230

Qy        206 FCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVV---VRIRIFWLLHTSG 262
              |    |  ::| | :   |  :||:  : :|  |: ||||||::     :  |||
Db        231 FAIVSIGLTIRNRGLGGQAGPQRAMRVLAMVVAVYTICFLPSIIFGMASMVAFWL----- 285

Qy        263 TQNCEVYRSVDLA---FFITLSFTYMNSMLDPVVYYFSSPSF 301
                  ||:||    |  :|:|||:||:||||:| ||||:|
Db        286 ----SACRSLDLCTQLFHGSLAFTYLNSVLDPVLYCFSSPNF 323


RESULT 12
Q8TDS5
ID   Q8TDS5      PRELIMINARY;      PRT;   423 AA.
AC   Q8TDS5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   G-protein coupled receptor TG1019.
GN   Name=GPCR; Synonyms=OXER1, tg1019;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22191290; PubMed=12065583; DOI=10.1074/jbc.M203194200;
RA   Hosoi T., Koguchi Y., Sugikawa E., Chikada A., Ogawa K., Tsuda N.,
RA   Suto N., Tsunoda S., Taniguchi T., Ohnuki T.;
RT   "Identification of a Novel Human Eicosanoid Receptor Coupled to
RT   Gi/o.";
RL   J. Biol. Chem. 277:31459-31465(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RA   Strausberg R.;
```

```
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR   EMBL; AB083630; BAB89343.1; -.
DR   EMBL; AB083055; BAC11806.2; -.
DR   EMBL; BC063549; AAH63549.1; -.
DR   GO; GO:0050648; F:5(S)-hydroxyperoxy-6E,8Z,11Z,14Z-icosatetra. . .; NAS.
DR   GO; GO:0050647; F:5-hydroxy-6E,8Z,11Z,14Z-icosatetraenoic aci. . .; NAS.
DR   GO; GO:0050646; F:5-oxo-6E,8Z,11Z,14Z-icosatetraenoic acid bi. . .; NAS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; NAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS.
DR   GO; GO:0030817; P:regulation of cAMP biosynthesis; IDA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237;.G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transmembrane.
SQ   SEQUENCE   423 AA;  45810 MW;  72ADA9F43A9EC051 CRC64;

  Query Match             27.1%;  Score 563;  DB 2;  Length 423;
  Best Local Similarity   41.8%;  Pred. No. 5.2e-31;
  Matches  118;  Conservative   52;  Mismatches   88;  Indels   24;  Gaps    5;

Qy         30 LPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVR 89
              | |:| |||: ||:|| |||:||| | : | |: :|| :|  |||||  ||  :| |:
Db         95 LAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFLLISNLPLRVDYYLL 154

Qy         90 RWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISC 149
                 |:||   |:: |||| :|  |::||| :|::|| :|| ||| |:: |   || ::
Db        155 HETWRFGAAACKVNLFMLSTNRTASVVFLTAIALNRYLKVVQPHHVLSRASVGAAARVAG 214

Qy        150 LLWGITIGLTVHLLKKKMPIQNGGANLCSSFSI----CHTFQWHEAMFLLEFFLPLGIIL 205
               ||   : |  |||     :       | |: :      : :||:|::|||||||| :||
Db        215 GLWVGILLLNGHLL-----LSTFSGPSCLSYRVGTKPSASLRWHQALYLLEFFLPLALIL 269

Qy        206 FCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVV---VRIRIFWLLHTSG 262
              |    |  ::| | :   |  :||:  : :|  |: ||||||::     :  |||
Db        270 FAIVSIGLTIRNRGLGGQAGPQRAMRVLAMVVAVYTICFLPSIIFGMASMVAFWL----- 324

Qy        263 TQNCEVYRSVDLA---FFITLSFTYMNSMLDPVVYYFSSPSF 301
                  ||:||    |  :|:|||:||:||||:| ||||:|
Db        325 ----SACRSLDLCTQLFHGSLAFTYLNSVLDPVLYCFSSPNF 362


RESULT 13
Q9NQ20
ID   Q9NQ20      PRELIMINARY;      PRT;   319 AA.
AC   Q9NQ20;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   BA517H2.2 (G protein-coupled receptor 31).
GN   Name=GPR31;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Almeida J.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL121935; CAB99329.1; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   319 AA;  35074 MW;  2ACD0350AD7FB53A CRC64;

  Query Match             23.9%;  Score 496.5;  DB 2;  Length 319;
  Best Local Similarity   36.4%;  Pred. No. 1.5e-26;
  Matches  110;  Conservative   56;  Mismatches  111;  Indels   25;  Gaps    5;

Qy         33 VLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRWD 92
              :|||   ||||| :||| | | :: ||   ::| |||:|| ||  |||||   |:
Db         20 LLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAACLPFLAAFYLSLQA 79

Qy         93 WKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLW 152
              |  | : |  : |:| ::|   : ||  ||:||| |||||   :| :| : |  :| |:|
Db         80 WHLGRVGCWALHFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNLLSPQAALGVSGLVW 139

Qy        153 GITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQ----------WHEAMFLLEFFLPLG 202
               : : ||   |       ||         : ||:|           | ||:  |:| || |
Db        140 LLMVALTCPGLLISEAAQNS--------TRCHSFYSRADGSFSIIWQEALSCLQFVLPFG 191

Qy        203 IILFCSARIIWSL--RQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLHT 260
              :|:||:| || :|  | |: ::  |::||   : :| ::| :|||  : |:    |:|
Db        192 LIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLARV----LMHI 247

Qy        261 -SGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQRKMTG 319
                  :|    :|     :| | ||::|:|:|||| ||||:| : :  : :    :
Db        248 FQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRVFHTLRGKGQAA 307

Qy        320 EP 321
               ||
Db        308 EP 309


RESULT 14
GP31_HUMAN
ID   GP31_HUMAN     STANDARD;      PRT;   319 AA.
AC   O00270;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Probable G protein-coupled receptor GPR31.
GN   Name=GPR31;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=97349123; PubMed=9205127; DOI=10.1006/geno.1997.4754;
RA   Zingoni A., Rocchi M., Storlazzi C.T., Bernardini G., Santoni A.,
RA   Napolitano M.;
RT   "Isolation and chromosomal localization of GPR31, a human gene
RT   encoding a putative G protein-coupled receptor.";
RL   Genomics 42:519-523(1997).
CC   -!- FUNCTION: Orphan receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U65402; AAC51375.1; -.
DR   Genew; HGNC:4486; GPR31.
DR   MIM; 602043; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
```

```
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane.
FT   DOMAIN        1     16       Extracellular (Potential).
FT   TRANSMEM     17     37       1 (Potential).
FT   DOMAIN       38     52       Cytoplasmic (Potential).
FT   TRANSMEM     53     73       2 (Potential).
FT   DOMAIN       74     91       Extracellular (Potential).
FT   TRANSMEM     92    110       3 (Potential).
FT   DOMAIN      111    131       Cytoplasmic (Potential).
FT   TRANSMEM    132    152       4 (Potential).
FT   DOMAIN      153    180       Extracellular (Potential).
FT   TRANSMEM    181    201       5 (Potential).
FT   DOMAIN      202    219       Cytoplasmic (Potential).
FT   TRANSMEM    220    240       6 (Potential).
FT   DOMAIN      241    265       Extracellular (Potential).
FT   TRANSMEM    266    284       7 (Potential).
FT   DOMAIN      285    319       Cytoplasmic (Potential).
FT   CARBOHYD      5      5       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   319 AA;  35079 MW;  7A4F164CD9C969DD CRC64;

  Query Match             23.8%;  Score 494.5;  DB 1;  Length 319;
  Best Local Similarity   36.1%;  Pred. No. 2.1e-26;
  Matches  109;  Conservative   57;  Mismatches  111;  Indels   25;  Gaps    5;

Qy         33 VLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRWD 92
              :||||   ||||| :||| | | :: ||   ::| |||:|| ||  |||||   |:
Db         20 LLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAACLPFLAAFYLSLQA 79

Qy         93 WKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLW 152
              |  | :  :  |:| ::|   : ||  ||:||| |||||   :| :| :  :| |:|
Db         80 WHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNLLSPQAALGVSGLVW 139

Qy        153 GITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQ----------WHEAMFLLEFFLPLG 202
               : : ||   |       ||         : ||:|           | ||:  |:| || |
Db        140 LLMVALTCPGLLISEAAQNS--------TRCHSFYSRADGSFSIIWQEALSCLQFVLPFG 191

Qy        203 IILFCSARIIWSL--RQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLHT 260
              :|:||:| || :|  | |: ::  |::||   : :| ::| :||||  : |:    |:|
Db        192 LIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLARV----LMHI 247

Qy        261 -SGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQRKMTG 319
               :|    :|     :| | ||::|:::|||| |||||: : :  : :    :
Db        248 FQNLGSCRALCAVAHTSDVTGSLTYLHSVVNPVVYCFSSPTFRSSYRRVFHTLRGKGQAA 307

Qy        320 EP 321
              ||
Db        308 EP 309


RESULT 15
Q9JLS1
ID   Q9JLS1      PRELIMINARY;      PRT;   319 AA.
AC   Q9JLS1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   G protein coupled receptor.
GN   Name=Tcp10c;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99431663; PubMed=10501965;
RA   Schimenti J.C.;
RT   "ORFless, intronless, and mutant transcription units in the mouse t
RT   complex responder (Tcr) locus.";
RL   Mamm. Genome 10:969-976(1999).
DR   EMBL; AF140708; AAF26668.1; -.
DR   MGD; MGI:98543; Tcp10c.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   319 AA;  35551 MW;  571F6DFB485BD7C4 CRC64;

  Query Match             23.1%;  Score 481;  DB 2;  Length 319;
  Best Local Similarity   35.7%;  Pred. No. 1.8e-25;
  Matches  109;  Conservative   61;  Mismatches  111;  Indels   24;  Gaps    7;

Qy         33 VLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRWD 92
              :| || : ||:|| :||| | : || ||   ::|||| ||| ||   :||    |::
Db         20 MLTLECVLGLMGNAVALWTFFYRLKVWKPYAVYLFNLVVADLLLATSVPFFAAFYLKGKT 79

Qy         93 WKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLW 152
              || | :||:|:||:|| :    : ||  ||:|||  ||||   :| :| | |  || |:|
Db         80 WKLGHMPCQLLLFLLAFSCGVGVAFLMTVALDRYLHVVHPRLRVNLLSLRAAWGISSLIW 139

Qy        153 GITIGLTVHLLKKKMPIQNGGANLCSSF---------SICHTFQWHEAMFLLEFFLPLGI 203
               : : ||   |       ||  :  | ||         : |       | :| |:  || |:
Db        140 LLMVVLTPQNLLTCRTTQN--STECPSFYPTGGTKAIATC-----QEVLFFLQVLLPFGL 192

Qy        204 ILFCSARIIWSLRQR--QMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLHT- 260
              | ||:: :| :|::|  : |:   |:||   : :: ::| :||||||: |:    |:|
Db        193 ISFCNSGLIRTLQKRLSESDKQPTIRRARVLVAIMLLLFGLCFLPSVLTRV----LVHIF 248

Qy        261 SGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQRKMTGE 320
              ::| | :::  |  | | | ::| | | :| ||:|:| : :  ::     |:  |
Db        249 QEFKSCSVQQAIMRASDIAGSLTCLHSTLSPAIYCFSNPAFTHSYRKVLKSLRGRRKAAE 308

Qy        321 -PDNN 324
               | :|
Db        309 SPSDN 313


Search completed: October 20, 2005, 06:04:15
Job time : 61 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 20, 2005, 05:56:35 ; Search time 68 Seconds
(without alignments)
2201.122 Million cell updates/sec

Title: US-10-800-249-2
Perfect score: 2081
Sequence: 1 MNRHHLQDHFLEIDKKNCCV.....KGHCHQEPASLEKQLGCCIE 387

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2081	100.0	387	8	ADT08043	Adt08043 Human G-p
2	1996	95.9	387	5	AAU77992	Aau77992 Human inf
3	1996	95.9	387	5	ADJ63768	Adj63768 Human G p
4	1996	95.9	387	7	ADF28984	Adf28984 Human G p
5	1995	95.9	387	6	ABR48195	Abr48195 Human bla
6	1995	95.9	387	7	ADN38906	Adn38906 Cancer/an
7	1995	95.9	387	8	ADQ60130	Adq60130 Human G-p
8	1995	95.9	625	7	ADF70463	Adf70463 Orphan re
9	1990	95.6	387	3	AAY90637	Aay90637 Human G p
10	1990	95.6	387	5	ABP54318	Abp54318 Human G p
11	1990	95.6	387	5	ABB98163	Abb98163 Human HM7
12	1990	95.6	387	5	AAU79041	Aau79041 Human G p
13	1990	95.6	387	6	ABP81898	Abp81898 Human G p
14	1990	95.6	387	7	ADC22627	Adc22627 Human G p
15	1990	95.6	387	7	ADH14100	Adh14100 Human HM7
16	1990	95.6	387	7	ADI17891	Adi17891 Human HM7
17	1990	95.6	387	7	ADN38910	Adn38910 Cancer/an
18	1990	95.6	387	8	ADN01996	Adn01996 Human inf
19	1990	95.6	387	8	ADO29488	Ado29488 Human GPC
20	1990	95.6	387	8	ADO59893	Ado59893 Human HM-
21	1990	95.6	387	8	ADO32541	Ado32541 hRUP38 re
22	1990	95.6	387	8	ADR43757	Adr43757 Human HM7
23	1990	95.6	387	8	ADP23835	Adp23835 PRO polyp
24	1990	95.6	387	8	ADS17050	Ads17050 Human 311
25	1990	95.6	387	8	ADT08044	Adt08044 Human G-p
26	1988	95.5	387	3	AAY90672	Aay90672 Human mut
27	1988	95.5	387	7	ADC22741	Adc22741 Human G p
28	1988	95.5	387	7	ADH14214	Adh14214 Mutated h
29	1988	95.5	387	8	ADM46114	Adm46114 Human 5-o
30	1935	93.0	362	6	ABG72358	Abg72358 Human orp
31	1935	93.0	363	2	AAW94654	Aaw94654 G-protein
32	1935	93.0	363	4	AAU04379	Aau04379 Human G-p
33	1935	93.0	363	7	ADC86215	Adc86215 Human GPC
34	1935	93.0	363	7	ADL96482	Adl96482 Human G p
35	1935	93.0	363	7	ADN38908	Adn38908 Cancer/an
36	1935	93.0	363	8	ADM46118	Adm46118 Human 5-o
37	1935	93.0	363	8	ADN41887	Adn41887 Amino aci
38	1935	93.0	363	8	ADO05575	Ado05575 Human hRU
39	1935	93.0	363	8	ADP04973	Adp04973 Human HM7
40	1935	93.0	363	8	ADO32543	Ado32543 hRUP25 re
41	1935	93.0	363	8	ADR37504	Adr37504 Human HM7
42	1930	92.7	363	5	AAU77993	Aau77993 Human inf
43	1930	92.7	363	5	ADJ63782	Adj63782 Human G p
44	1930	92.7	363	7	ADF28998	Adf28998 Human G p
45	1918.5	92.2	362	8	ADT08045	Adt08045 Human GPC

ALIGNMENTS

RESULT 1
ADT08043
ID ADT08043 standard; protein; 387 AA.
XX
AC ADT08043;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human G-protein coupled receptor HGPRBMY74, SEQ ID 2.
XX
KW GPCR; HGPRBMY74; G-protein coupled receptor; immunosuppressive;
KW antilipaemic; antidiabetic; anorectic; antiinflammatory; cardiant;
KW antirheumatic; antiarthritic; antiarteriosclerotic; osteopathic;
KW pulmonary; antiasthmatic; cytostatic; dermatological; antipsoriatic;
KW ophthalmological; human; receptor.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 38. .54
FT /note = transmembrane domain TM1
FT Domain 64. .84
FT /note = transmembrane domain TM2
FT Domain 95. .123
FT /note = transmembrane domain TM3
FT Domain 144. .163
FT /note = transmembrane domain TM4
FT Domain 191. .209
FT /note = transmembrane domain TM5
FT Domain 229..250
FT /note = transmembrane domain TM6
FT Domain 274. .292
FT /note = transmembrane domain TM7
XX
PN WO2004083388-A2.
XX
PD 30-SEP-2004.
XX
PF 12-MAR-2004; 2004WO-US007618.
XX
PR 14-MAR-2003; 2003US-0454942P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Ramanathan CS, Feder JN;
XX
DR WPI; 2004-691038/67.
DR N-PSDB; ADT08042.

```
XX
PT   New nucleic acid molecules encoding HGPRBMY74 polypeptides of the G-
PT   protein coupled receptor superfamily, useful for diagnosing, treating, or
PT   ameliorating dyslipidemia, diabetes, or inflammatory disorders.
XX
PS   Claim 5; Fig 1A-B; 332pp; English.
XX
CC   The invention relates to an isolated human G-protein coupled receptor
CC   (GPCR), HGPRBMY74 and encoding polynucleotides. The HGPRBMY74 polypeptide
CC   can be expressed by standard recombinant methodology. The nucleic acid
CC   molecules, polypeptides, modulators and methods are useful for
CC   diagnosing, treating or ameliorating a pathological condition, e.g. a
CC   disorder related to aberrant G-protein coupled signaling; a disorder
CC   related to aberrant nicotinic acid dependent-G-protein coupled signaling;
CC   a disorder related to aberrant cell cycle regulation; cardiovascular
CC   disorders; an immune disorder; disorders associated with aberrant
CC   nicotinic acid utilization; disorders associated with aberrant nicotinic
CC   acid absorption; disorders associated with aberrant in nicotinic acid
CC   responses; dyslipidaemia; diabetic dyslipidaemia; mixed dyslipidaemia;
CC   hypercholesteremia; hypertriglyceridemia; type II diabetes mellitus; type
CC   I diabetes; insulin resistance; hyperlipidaemia; obesity; anorexia
CC   nervosa; disease or disorders known to be associated with HM74; disease
CC   or disorders known to be associated with HM74A; heart failure;
CC   atherosclerosis; arteriosclerosis; hypertriglyceridemia; inflammatory
CC   disorders; arthritis; rheumatoid arthritis; osteoarthritis; prosthetic
CC   joint failure; gastrointestinal tract disorders; ulcerative colitis;
CC   Crohn's disease; inflammatory bowel disorder; gastritis; mucosal
CC   inflammation; enteropathy provoked by non-steroidal anti-inflammatory
CC   drugs; lung disorders; adult respiratory distress syndrome; asthma;
CC   cystic fibrosis; chronic obstructive pulmonary disease; myocarditis;
CC   multiple sclerosis; inflammation associated with diabetes mellitus;
CC   glomerulonephritis; dermatitis; psoriasis; eczema; urticaria; burn injury
CC   ; glaucoma; organ rejection; systemic lupus erythematosus; sepsis;
CC   ischaemic heart disease; disorders associated with aberrant lipolysis;
CC   stroke; dyslipidaemia; disorders associated with below average levels of
CC   high density lipoprotein (HDL); disorders associated with above average
CC   levels of very low density lipoprotein (VLDL); disorders associated with
CC   above average levels of low density lipoprotein (LDL); and disorders
CC   associated with above average levels of cholesterol. The present sequence
CC   represents a human GPCR, HGPRBMY74.
XX
SQ   Sequence 387 AA;

  Query Match             100.0%;  Score 2081;  DB 8;  Length 387;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-207;
  Matches  387;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 2
AAU77992
ID   AAU77992 standard; protein; 387 AA.
XX
AC   AAU77992;
XX
DT   02-JUL-2002  (first entry)
XX
DE   Human inflammation-associated GPCR EX20 polypeptide.
XX
KW   Human; inflammation-associated G-protein coupled receptor; GPCR; EX20;
KW   inflammatory disease; asthma; adult respiratory distress syndrome; ARDS;
KW   chronic obstructive pulmonary disease; COPD; bronchitis; emphysema;
KW   pneumoconiosis; neutrophil; eosinophil related disorder; airway;
KW   lung-related disorder; rheumatoid arthritis; inflammatory bowel disease;
KW   ulcerative colitis; skin disease; eczematous dermatitis; receptor.
XX
OS   Homo sapiens.
XX
PN   WO200213845-A2.
XX
PD   21-FEB-2002.
XX
PF   16-AUG-2001; 2001WO-EP009466.
XX
PR   18-AUG-2000; 2000US-00641653.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Jarai G,  Yousefi S;
XX
DR   WPI; 2002-329542/36.
DR   N-PSDB; ABK47759.
XX
PT   New pharmaceutical composition comprising EX20 polypeptide, EX20
PT   polynucleotide, antibodies against EX20 polypeptide, antisense
PT   oligonucleotides against EX20 polynucleotide, useful for treating
PT   inflammatory disease.
XX
PS   Claim 2; Page 31-32; 36pp; English.
XX
CC   The present invention relates to human inflammation-associated G-protein
CC   coupled receptor (GPCR) EX20 polypeptide and the polynucleotide sequence
CC   encoding it. A pharmaceutical composition comprising EX20 polypeptide, a
CC   variant of EX20, an antibody which immunoreacts with EX20, a
CC   polynucleotide encoding EX20 or an antisense oligonucleotide comprising a
CC   nucleotide sequence complementary to EX20 can be used in diagnostic and
CC   therapeutic applications for treating an inflammatory disease. Such
CC   inflammatory diseases include asthma, adult respiratory distress syndrome
CC   (ARDS), chronic obstructive pulmonary disease (COPD) including chronic
CC   bronchitis, emphysema, pneumoconiosis, neutrophil or eosinophil related
CC   disorders, airway and lung-related disorders, rheumatoid arthritis,
CC   inflammatory bowel disease, ulcerative colitis, and skin diseases such as
CC   eczematous dermatitis. The present sequence represents human inflammation
CC   -associated GPCR EX20 polypeptide
XX
SQ   Sequence 387 AA;

  Query Match             95.9%;  Score 1996;  DB 5;  Length 387;
  Best Local Similarity   96.1%;  Pred. No. 4.1e-198;
  Matches  372;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              ||||||||||||||||||:|| |||| ||||||||||:||| ||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120
```

```
Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||||:||||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGTANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIHIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
```

```
RESULT 3
ADJ63768
ID   ADJ63768 standard; protein; 387 AA.
XX
AC   ADJ63768;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human  G protein-coupled receptor EX20 #1.
XX
KW   Human; receptor; G protein-coupled receptor; EX20; GPCR;
KW   inflammatory disease; obstructive airway disease; asthma;
KW   chronic obstructive pulmonary disease; neutrophil related disorder;
KW   eosinophil related disorder; inflammatory skin disease;
KW   eczematous dermatitis.
XX
OS   Homo sapiens.
XX
PN   US2004038895-A1.
XX
PD   26-FEB-2004.
XX
PF   14-JUL-2003; 2003US-00619141.
XX
PR   18-AUG-2000; 2000US-00641653.
PR   18-AUG-2000; 2000US-0421154P.
PR   15-AUG-2001; 2001US-00930334.
XX
PA   (JARA/) JARAI G.
PA   (YOUS/) YOUSEFI S.
XX
PI   Jarai G,  Yousefi S;
XX
DR   WPI; 2002-329542/36.
DR   N-PSDB; ADJ63767.
XX
PT   New pharmaceutical composition comprising EX20 polypeptide, EX20
PT   polynucleotide, antibodies against EX20 polypeptide, antisense
PT   oligonucleotides against EX20 polynucleotide, useful for treating
PT   inflammatory disease.
XX
PS   Claim 1; SEQ ID NO 2; 17pp; English.
XX
CC   The invention relates to a pharmaceutical composition, comprising an
CC   inflammation-associated G protein-coupled receptor (GPCR) gene designated
CC   EX20 (e.g. the cDNAs appearing as ADJ63767 or ADJ63781, EX20 polypeptide
CC   (appearing as ADJ63768 and ADJ63782, an anti-EX20 antibody or an
CC   antisense oligonucleotide against EX20 expression. Also included are an
CC   antibody which is immunoreactive with a polypeptide, an antisense
CC   oligonucleotide comprising a nucleotide sequence complementary to that of
CC   the polynucleotide, a polynucleotide probe comprising at least 15
CC   contiguous nucleotides of the polynucleotide or its complement, a method
CC   of treating an inflammatory disease, a method of detecting the presence
CC   of a polynucleotide in a cell or tissue, a method of determining whether
CC   a subject has an inflammatory disease, a method of monitoring treatment
CC   of a subject having an inflammatory disease, a pair of oligonucleotides
CC   useful as primers for amplification of a fragment of the polynucleotide
CC   (each oligonucleotide of the pair is at least 15 nucleotides in length
CC   and the pair having sequences so that when used in a polymerase chain
CC   reaction with human genomic DNA or a suitable human cDNA target, they
CC   result in synthesis of a DNA fragment containing a part or all of the
CC   nucleotide sequence of the polynucleotide) and a method of identifying a
CC   substance suitable for use in the treatment of an inflammatory disease.
CC   Treating an inflammatory disease comprises administering to a subject an
CC   amount of the polypeptide, polynucleotide, antibody or antisense
CC   oligonucleotide (the disease is an inflammatory or obstructive airway
CC   disease, preferably asthma or chronic obstructive pulmonary disease). The
CC   polypeptide, polynucleotide, antibody or antisense oligonucleotide is
CC   useful for the preparation of a medicament for the treatment of
CC   inflammatory diseases. It is also useful for treating neutrophil or
CC   eosinophil related disorders and inflammatory skin diseases including
CC   eczematous dermatitis. The present sequence represents EX20.
XX
SQ   Sequence 387 AA;
```

```
  Query Match             95.9%;  Score 1996;  DB 5;  Length 387;
  Best Local Similarity   96.1%;  Pred. No. 4.1e-198;
  Matches  372;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||||||:|| |||| ||||||||||:||| |||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGTANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIHIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
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```
RESULT 4
ADF28984
ID   ADF28984 standard; protein; 387 AA.
XX
AC   ADF28984;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human G protein-coupled receptor (GPCR) EX20 polypeptide #1.
XX
KW   Human; G protein-coupled receptor; GPCR; EX20; inflammatory disease;
KW   obstructive airways disease; asthma;
KW   chronic obstructive pulmonary disease; COPD;
KW   respiratory tract inflammation; bronchitis; emphysema;
KW   adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KW   inflammatory bowel disease; IBD; ulcerative colitis;
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KW   primary sclerosing cholangitis; Crohn's disease; antiinflammatory;
KW   antiasthmatic; receptor.
XX
OS   Homo sapiens.
XX
PN   US2003078218-A1.
XX
PD   24-APR-2003.
XX
PF   15-AUG-2001; 2001US-00930334.
XX
PR   15-AUG-2001; 2001US-00930334.
XX
PA   (JARA/) JARAI G.
PA   (YOUS/) YOUSEFI S.
XX
PI   Jarai G,  Yousefi S;
XX
DR   WPI; 2003-635083/60.
DR   N-PSDB; ADF28983.
XX
PT   New pharmaceutical composition comprising a polypeptide, polynucleotide,
PT   antibody and/or antisense oligonucleotide, useful for diagnosing and/or
PT   treating an inflammatory and/or obstructive airways disease.
XX
PS   Claim 1; SEQ ID NO 2; 18pp; English.
XX
CC   The invention relates to a pharmaceutical composition comprising active
CC   ingredients of a human G protein-coupled receptor (GPCR) polypeptide, a
CC   polynucleotide encoding the polypeptide, an antibody which is
CC   immunoreactive with the polypeptide or an antisense oligonucleotide
CC   comprising a nucleotide sequence complementary to the polypeptide. The
CC   composition is used for treating an inflammatory disease or an
CC   obstructive airways disease, e.g. asthma, chronic obstructive pulmonary
CC   disease (COPD), respiratory tract inflammation, bronchitis, emphysema,
CC   adult respiratory distress syndrome (ARDS), rheumatoid arthritis,
CC   inflammatory bowel disease (IBD), ulcerative colitis, primary sclerosing
CC   cholangitis and Crohn's disease. The level of expression of the
CC   polynucleotide is used for diagnosing and monitoring inflammatory
CC   disease. The expression and/or activity of the polypeptide is also used
CC   for monitoring inflammatory disease and for screening of substrates
CC   useful for treating inflammatory disease. This sequence represents a
CC   human GPCR polypeptide, EX20.
XX
SQ   Sequence 387 AA;

  Query Match             95.9%;  Score 1996;  DB 7;  Length 387;
  Best Local Similarity   96.1%;  Pred. No. 4.1e-198;
  Matches  372;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              ||||||||||||||||||||:|| |||| |||||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| ||||||||||:|||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGTANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIHIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 5
ABR48195
ID   ABR48195 standard; protein; 387 AA.
XX
AC   ABR48195;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Human bladder cancer associated protein sequence SEQ ID NO:108.
XX
KW   Human; bladder cancer; cytostatic; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2003003906-A2.
XX
PD   16-JAN-2003.
XX
PF   03-JUL-2002; 2002WO-US021338.
XX
PR   03-JUL-2001; 2001US-0302814P.
PR   03-AUG-2001; 2001US-0310099P.
PR   08-NOV-2001; 2001US-0343705P.
PR   13-NOV-2001; 2001US-0350666P.
PR   12-APR-2002; 2002US-0372246P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Mack DH,  Aziz N;
XX
DR   WPI; 2003-201532/19.
DR   N-PSDB; ACC51008.
XX
PT   Detecting a bladder cancer-associated transcript in a cell from a
PT   patient, comprises contacting a biological sample from the patient with a
PT   bladder cancer-associated polynucleotide or antibody.
XX
PS   Claim 10; Page 269; 307pp; English.
XX
CC   The present invention describes a method for detecting a bladder cancer-
CC   associated transcript in a cell from a patient. The method comprises
CC   contacting a biological sample from the patient with a polynucleotide
CC   that selectively hybridises to a sequence that is 80 % identical to a
CC   table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
CC   encode the human bladder cancer-associated proteins given in ABR48146 to
CC   ABR48242). Bladder cancer-associated sequences from the present invention
CC   have cytostatic activities, and can be used in antisense gene therapy and
CC   in vaccine production. The method can be used for detecting a bladder
CC   cancer-associated transcript in a cell from a patient. The method is
CC   useful in diagnosing or treating bladder cancer and in screening for
CC   compounds that modulate bladder cancer, such as hormones or antibodies.
CC   The nucleic acid molecules from the present invention may be used in
CC   various screening and diagnostic methods, and for gene therapy, vaccine
CC   and/or antisense/inhibition applications
XX
SQ   Sequence 387 AA;

  Query Match             95.9%;  Score 1995;  DB 6;  Length 387;
  Best Local Similarity   96.1%;  Pred. No. 5.2e-198;
  Matches  372;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              ||||||||||||||||||||:|| |||| |||||||||||:||| ||||||||||||||
```

```
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              |||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
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```
RESULT 6
ADN38906
ID   ADN38906 standard; protein; 387 AA.
XX
AC   ADN38906;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:224.
XX
KW   Human; differential expression; cancer; angiogenic disorder;
KW   fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW   inflammatory disease; autoimmune disease;
KW   retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW   detection; diagnosis; prognosis; drug screening; drug targeting;
KW   wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW   vulnerary; gene therapy; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO2003042661-A2.
XX
PD   22-MAY-2003.
XX
PF   13-NOV-2002; 2002WO-US036810.
XX
PR   13-NOV-2001; 2001US-0350666P.
PR   21-NOV-2001; 2001US-0332464P.
PR   29-NOV-2001; 2001US-0334393P.
PR   03-DEC-2001; 2001US-0335394P.
PR   14-DEC-2001; 2001US-0340376P.
PR   08-JAN-2002; 2002US-0347211P.
PR   10-JAN-2002; 2002US-0347349P.
PR   08-FEB-2002; 2002US-0355250P.
PR   13-FEB-2002; 2002US-0356714P.
PR   20-FEB-2002; 2002US-0359077P.
PR   29-MAR-2002; 2002US-0368809P.
PR   04-APR-2002; 2002US-0370110P.
PR   12-APR-2002; 2002US-0372246P.
PR   05-JUN-2002; 2002US-0386614P.
PR   16-JUL-2002; 2002US-0396839P.
PR   22-JUL-2002; 2002US-0397775P.
PR   22-JUL-2002; 2002US-0397845P.
PR   09-SEP-2002; 2002US-0409450P.
XX
PA   (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI   Afar D,  Aziz N,  Ginsburg WM,  Gish KC,  Glynne R,  Hevezi PA;
PI   Mack DH,  Murray R,  Watson SR,  Wilson KE,  Zlotnik A;
XX
DR   WPI; 2003-468649/44.
DR   N-PSDB; ADN38905.
XX
PT   Determining the presence or absence of a pathological cell in a patient,
PT   useful for diagnosing, prognosing or treating cancer, comprises detecting
PT   a nucleic acid in a biological sample.
XX
PS   Claim 12; SEQ ID NO 224; 1385pp; English.
XX
CC   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC   whose expression is upregulated or downregulated in specific cancers or
CC   other diseases such as angiogenic or fibrotic disorders, and to methods
CC   of determining the presence or absence of a pathological cell in a
CC   patient by detecting a nucleic acid at least 80% identical to those of
CC   the invention or by detecting a polypeptide of the invention. The
CC   invention also relates to expression vectors and host cells comprising a
CC   nucleic acid of the invention; antibodies which specifically bind a
CC   polypeptide of the invention; use of such antibodies for drug targeting;
CC   and methods of screening for modulators of activity or expression of the
CC   polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC   antibodies and methods are useful for diagnosing, prognosing and treating
CC   cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC   atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC   neovascularistaion syndromes, scarring and uterine fibroids. They may
CC   also be useful in wound healing and in contraception. The present
CC   sequence represents a polypeptide of the invention.
XX
SQ   Sequence 387 AA;
```

```
  Query Match           95.9%;  Score 1995;  DB 7;  Length 387;
  Best Local Similarity  96.1%;  Pred. No. 5.2e-198;
  Matches  372;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||||:|| |||| |||||||||||:||| |||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              |||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
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```
RESULT 7
ADQ60130
ID   ADQ60130 standard; protein; 387 AA.
XX
AC   ADQ60130;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Human G-protein coupled receptor protein (GPCR) HM74 protein.
XX
KW   G-protein coupled receptor; GPCR ligand binding; N-formyl-L-methionine;
```

KW antiinflammatory; antiallergic; antirheumatic; antiarthritic;
KW osteopathic; dermatological; immunosuppressive; immunodeficiency;
KW allergy; rheumatism; osteoarthritis; lupus erythematosus; human; HM74;
KW receptor.
XX
OS Homo sapiens.
XX
PN JP2004198202-A.
XX
PD 15-JUL-2004.
XX
PF 17-DEC-2002; 2002JP-00365684.
XX
PR 17-DEC-2002; 2002JP-00365684.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
DR WPI; 2004-513647/49.
DR N-PSDB; ADQ60131.
XX
PT Screening compound or its salt that affects binding of ligand of G-
PT protein coupled receptor protein (HM74) with HM74, or its partial peptide
PT or salt, by using N-formyl-L-methionine.
XX
PS Claim 1; SEQ ID NO 1; 51pp; Japanese.
XX
CC The invention relates to a novel method for screening a compound, or its
CC salt, that affects the binding of the ligand of G-protein coupled
CC receptor (GPCR) HM74 with HM74, or its partial peptide or salt, by using
CC N-formyl-L-methionine, where HM74 has a fully defined sequence as given
CC in the specification. The method of the invention has antiinflammatory,
CC antiallergic, antirheumatic, antiarthritic, osteopathic, dermatological
CC and immunosuppressive activities and may be useful for treating
CC immunodeficiency disorders, such as allergy, rheumatism, osteoarthritis
CC or lupus erythematosus. The current sequence is that of the human G-
CC protein coupled receptor protein (GPCR) HM74 protein of the invention.
XX
SQ Sequence 387 AA;

Query Match 95.9%; Score 1995; DB 8; Length 387;
Best Local Similarity 96.1%; Pred. No. 5.2e-198;
Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

```
Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| ||||||||||:||| |||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||:||||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              |||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
```

RESULT 8

ADF70463
ID ADF70463 standard; protein; 625 AA.
XX
AC ADF70463;
XX
DT 12-FEB-2004 (first entry)
XX
DE Orphan receptor ligand-related human protein SeqID86.
XX
KW ligand; orphan receptor protein; fusion protein; fluorescent protein;
KW cell expression; green fluorescent protein; GFP; GFP-1; wild-type GFP;
KW GFPuv; Enhanced GFP; EGFP; human.
XX
OS Homo sapiens.
XX
PN WO2003071272-A1.
XX
PD 28-AUG-2003.
XX
PF 21-FEB-2003; 2003WO-JP001901.
XX
PR 22-FEB-2002; 2002JP-00045728.
PR 23-JUL-2002; 2002JP-00213949.
PR 11-OCT-2002; 2002JP-00298237.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Hinuma S, Fujii R, Ogi K, Komatsu H, Kawamata Y, Hosoya M;
XX
DR WPI; 2003-697654/66.
DR N-PSDB; ADF70565.
XX
PT Transformation of cells with a fusion protein of an orphan receptor
PT protein with a fluorescent protein useful for identification of ligands
PT to the orphan receptor.
XX
PS Disclosure; SEQ ID NO 86; 594pp; Japanese.
XX
CC This invention relates to a novel method of identifying ligands to an
CC orphan receptor protein which comprises transforming cells with DNA
CC encoding a fusion protein of the orphan receptor with a fluorescent
CC protein, so that the fusion protein is expressed in the cells (or cell
CC membranes isolated from them) and contacting the cells with the potential
CC ligand to be tested. A suitable fluorescent protein for incorporation in
CC the fusion protein is green fluorescent protein (GFP), for example GFP-1,
CC wild-type GFP, GFPuv or Enhanced GFP (EGFP). The method is useful for the
CC identification of ligands binding to an orphan receptor protein.
XX
SQ Sequence 625 AA;

Query Match 95.9%; Score 1995; DB 7; Length 625;
Best Local Similarity 96.1%; Pred. No. 9.8e-198;
Matches 372; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

```
Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| ||||||||||:||| |||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||:||||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              |||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
```

```
Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 9
AAY90637
ID   AAY90637 standard; protein; 387 AA.
XX
AC   AAY90637;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human G protein-coupled receptor HM74.
XX
KW   G protein-coupled receptor; GPCR; constitutively active;
KW   intracellular loop 3; transmembrane domain 6; drug screening; agonist;
KW   antagonist.
XX
OS   Homo sapiens.
XX
PN   WO200022129-A1.
XX
PD   20-APR-2000.
XX
PF   12-OCT-1999;   99WO-US023938.
XX
PR   13-OCT-1998;   98US-00170496.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Behan DP,  Chalmers DT,  Liaw CW;
XX
DR   WPI; 2000-329165/28.
DR   N-PSDB; AAA30658.
XX
PT   Non-endogenous constitutively activated human G protein-coupled
PT   receptors, useful for identifying agonists for use as pharmaceutical
PT   agents.
XX
PS   Example 1; Page 185-187; 341pp; English.
XX
CC   The invention relates to constitutively active, non-endogenous versions
CC   of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC   AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC   and AAA30775-A30779). The mutant proteins of the invention contain a
CC   mutation in a portion of the protein comprising intracellular loop 3
CC   (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC   is substituted for an endogenous residue in IC3 at a position 16 amino
CC   acids N-terminal of an endogenous proline in TM6 to form a sequence X-
CC   (AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg or
CC   Ala, and is preferably Lys. When the endogenous residue at this position
CC   is Lys, this residue is replaced by His, Arg or preferably Ala. The 15
CC   amino acid stretch between the substituted amino acid and the Pro may be
CC   endogenous, non-endogenous, or a mixture of endogenous and non-endogenous
CC   residues. The constitutively active GPCRs are useful for identifying
CC   antagonists, agonists and partial agonists for use as pharmaceutical
CC   agents. The mutant proteins are also useful in research settings for
CC   elucidating the roles of the receptors in normal and diseased conditions.
CC   Antagonists for a particular GPCR are useful for treating diseases and
CC   disorders associated with that receptor. Because the novel mutant GPCRs
CC   are constitutively active, they can be used directly for screening of
CC   compounds without the need for endogenous ligands. The present sequence
CC   represents a human wild-type GPCR referred to in an exemplification of
CC   the invention
XX
SQ   Sequence 387 AA;
```

```
  Query Match             95.6%;  Score 1990;  DB 3;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 1.7e-197;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:|||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 10
ABP54318
ID   ABP54318 standard; protein; 387 AA.
XX
AC   ABP54318;
XX
DT   16-JAN-2003  (first entry)
XX
DE   Human G protein coupled receptor HM74 protein SEQ ID NO:8.
XX
KW   Human; G protein coupled receptor; GPCR; HGPRBMY27; antiinflammatory;
KW   antiinfertility; pulmonary; cytostatic; nephrotropic; hormonal;
KW   circulatory; gene therapy; inflammatory disorder; reproductive disorder;
KW   pulmonary disorder; cancer; renal disorder; connective tissue disorder;
KW   endocrine disorder.
XX
OS   Homo sapiens.
XX
PN   WO200272755-A2.
XX
PD   19-SEP-2002.
XX
PF   06-MAR-2002; 2002WO-US006796.
XX
PR   07-MAR-2001; 2001US-0273808P.
PR   27-MAR-2001; 2001US-0278983P.
XX
PA   (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI   Ramanathan C,  Feder J,  Mintier G,  Cacace A,  Barber L;
XX
DR   WPI; 2002-657945/70.
XX
PT   New polynucleotide encoding a human G-protein coupled receptor for
PT   preventing, treating, or ameliorating e.g. an inflammatory, reproductive,
PT   pulmonary, renal connective tissue, or endocrine disorder.
XX
PS   Disclosure; Fig 2A-B; 356pp; English.
XX
CC   The present invention describes a human G protein coupled receptor
```

```
CC   (GPCR), designated HGPRBMY27 (I). (I) has antiinflammatory,
CC   antiinfertility, pulmonary, cytostatic, nephrotropic, hormonal and
CC   circulatory activities, and can be used in gene therapy. (I) or the
CC   protein encoded by it can be used to prevent, treat, or ameliorate a
CC   medical condition, such as inflammatory disorders, reproductive
CC   disorders, pulmonary disorders, cancer, renal disorders, connective
CC   tissue disorders, endocrine disorders, or disorders involving aberrations
CC   in tubular tissues. They can also be used to diagnose a pathological
CC   condition or a susceptibility to (I). The protein can be used to screen
CC   for candidate compounds capable of modulating activity of a GPCR
CC   polypeptide. The present sequence represents a GPCR given in comparison
CC   with the HGPRBMY27 protein in the exemplification of the present
CC   invention
XX
SQ   Sequence 387 AA;

  Query Match             95.6%;  Score 1990;  DB 5;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 1.7e-197;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              ||||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              |||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 11
ABB98163
ID   ABB98163 standard; protein; 387 AA.
XX
AC   ABB98163;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Human HM74-like GPCR protein #2.
XX
KW   Human; HM74-like G protein coupled receptor; GPCR; antibacterial;
KW   fungicide; virucide; protozoacide; analgesic; cytostatic; antiasthmatic;
KW   hypertensive; hypotensive; antianginal; cardiant; osteopathic; anorectic;
KW   antiulcer; antiallergic; antiinflammatory; neuroprotective; neuroleptic;
KW   antiparkinsonian; anticonvulsant; nootropic; tranquiliser; antimanic;
KW   antidepressant; antidiabetic; cerebroprotective; antiarthritic;
KW   antilipemic; gynecological; depilatory; immunomodulator; bacterial;
KW   fungal; protozoan; viral; infection; human immunodeficiency virus;
KW   cancer; anorexia; asthma; central nervous system disease;
KW   cardiovascular disease; hypotension; hypertension; urinary retention;
KW   osteoporosis; obesity; ulcer; inflammation; allergy; multiple sclerosis;
KW   neurological disorder; dyskinesia; Parkinson's disease; manic depression;
KW   dementia; obesity; wasting disorder; stroke; osteoarthritis; respiratory;
KW   type 2 diabetes; thrombolic disease; reduced fertility; pregnancy;
KW   menstrual irregularities; hirsutism; stress incontinence; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200194385-A2.
XX
PD   13-DEC-2001.
XX
PF   05-JUN-2001; 2001WO-EP006380.
XX
PR   05-JUN-2000; 2000US-0208912P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Ramakrishnan S;
XX
DR   WPI; 2002-566439/60.
XX
PT   New human HM74-like G-protein coupled receptor polypeptide and
PT   polynucleotide, useful for treating cancer, cardiovascular disease,
PT   psychotic and neurological disorders, asthma, obesity and inflammation.
XX
PS   Disclosure; Fig 4; 105pp; English.
XX
CC   The invention relates to an isolated HM74-like G-protein coupled receptor
CC   (GPCR) polypeptide. Polypeptides and polynucleotides of the invention are
CC   useful for screening for agents which decrease the activity of HM74-like
CC   GPCR polypeptides. Compositions of the invention are useful for
CC   modulating the activity of HM74-like GPCR in a disease including
CC   bacterial, fungal, protozoan and viral infection, particularly human
CC   immunodeficiency viruses, cancer, anorexia, asthma, central nervous
CC   system disease, cardiovascular disease, hypotension, hypertension,
CC   urinary retention, osteoporosis, obesity, ulcer, inflammation, allergy,
CC   multiple sclerosis, neurological disorder and dyskinesias such as
CC   Parkinson's disease, manic depression, and dementia. The HM74-like GPCR
CC   gene or its portion or product are useful for treating obesity, wasting
CC   disorders, stroke, osteoarthritis, respiratory problems, type 2 diabetes,
CC   thrombolic disease, reduced fertility, complications of pregnancy,
CC   menstrual irregularities, hirsutism and stress incontinence. Polypeptides
CC   and polynucleotides of the invention may also be used in gene therapy.
CC   The current sequence represents a human HM74-like GPCR protein
XX
SQ   Sequence 387 AA;

  Query Match             95.6%;  Score 1990;  DB 5;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 1.7e-197;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              ||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              ||||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
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Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
```

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                    ||||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
```

RESULT 12
AAU79041
ID AAU79041 standard; protein; 387 AA.
XX
AC AAU79041;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human G protein-coupled receptor, HM74 receptor.
XX
KW Human; G protein-coupled; receptor; HM74; ILM receptor;
KW macrophage surface receptor; antiinflammatory; pulmonary;
KW chronic inflammatory airway disease; chronic bronchitis;
KW chronic obstructive pulmonary disease; COPD.
XX
OS Homo sapiens.
XX
PN WO200218938-A1.
XX
PD 07-MAR-2002.
XX
PF 23-AUG-2001; 2001WO-EP009727.
XX
PR 01-SEP-2000; 2000GB-00021484.
XX
PA (BOEH) BOEHRINGER INGELHEIM PHARMA KG.
XX
PI Jung B, Kraut N, Mueller S, Kistler B, Seither P, Quast K;
PI Weith A;
XX
DR WPI; 2002-315580/35.
DR N-PSDB; ABK48114.
XX
PT Determining an expression level of ILM (a macrophage surface receptor),
PT for the diagnosis or monitoring of chronic inflammatory airway disease,
PT comprises determining the level of the ILM receptor expressed in a
PT macrophage.
XX
PS Claim 7; Page 72-74; 79pp; English.
XX
CC The invention relates to determining an expression level of an ILM
CC receptor (macrophage surface receptor), comprises determining the level
CC of an ILM receptor expressed in a macrophage. Also included are a method
CC of determining whether a substance is an activator or an inhibitor of an
CC ILM receptor, involving applying the substance to a test system which
CC generates a measurable read-out upon modulation of the ILM receptor or an
CC ILM receptor function, a test system for determining whether a substance
CC is an activator or an inhibitor of an ILM receptor function,
CC characterised in that the receptor is involved in a chronic inflammatory
CC airway disease and where the receptor plays a role in mediating
CC inflammation comprising: (i) an ILM receptor; (ii) an expression vector
CC capable of expressing an ILM receptor in a cell; or (iii) a host cell
CC transformed with an expression vector capable of expressing the ILM
CC receptor and a substance determined to be an activator or inhibitor of an
CC ILM receptor. The methods are useful for the diagnosis or monitoring of a
CC chronic inflammatory airway disease, e.g. chronic bronchitis and chronic
CC obstructive pulmonary disease (COPD). The substance determined to be an
CC activator or inhibitor of an ILM receptor, is useful for treating the
CC diseases and for modulating an ILM receptor in a macrophage. The present
CC sequence is an ILM receptor which is differentially expressed and which
CC is involved in causing the induction and/or maintenance of the
CC hyperactive status of macrophages involved in an inflammatory process
XX
SQ Sequence 387 AA;

Query Match 95.6%; Score 1990; DB 5; Length 387;
Best Local Similarity 95.9%; Pred. No. 1.7e-197;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

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Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
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Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| || |||||||:||| ||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| ||||||||||||:|||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
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Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
```

RESULT 13
ABP81898
ID ABP81898 standard; protein; 387 AA.
XX
AC ABP81898;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human G protein-coupled receptor HM74 protein SEQ ID NO:281.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR N-PSDB; ABZ42745.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX

```
PS   Disclosure; Fig 1; 523pp; English.
XX
CC   The present invention describes antigenic peptides (I) comprising: (a)
CC   any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC   acids. Also described: (1) an assay for the detection of a particular G
CC   protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC   and (2) an isolated antibody having high specificity and high affinity or
CC   avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC   gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC   antibody against a particular GPCR, and in the production of specific
CC   antibodies. The peptides and antibodies are also useful for detecting the
CC   presence or absence of corresponding GPCRs. The antigenic peptides for
CC   GPCRs and antibodies are useful for diagnosing and designing drugs for
CC   treating immune-related diseases, growth-related diseases, cell
CC   regeneration-related disease, immunological-related cell proliferative
CC   diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC   atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC   osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC   inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC   disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC   anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC   loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC   hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC   any other disorder in which GPCRs are involved. The antibodies may be
CC   used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 387 AA;

  Query Match             95.6%;  Score 1990;  DB 6;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 1.7e-197;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 14
ADC22627
ID   ADC22627 standard; protein; 387 AA.
XX
AC   ADC22627;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human G protein-coupled receptor (GPCR) polypeptide #29.
XX
KW   Human; G protein-coupled receptor; GPCR; transmembrane-6 region; TM6;
KW   intracellular-3 region; IC3; receptor.
XX
OS   Homo sapiens.
XX
PN   US6555339-B1.
XX
PD   29-APR-2003.
XX
PF   13-OCT-1998;   98US-00170496.
XX
PR   14-APR-1997;   97US-00839449.
PR   14-APR-1998;   98US-00060188.
PR   26-JUN-1998;   98US-0090783P.
PR   07-AUG-1998;   98US-0095677P.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Liaw CW,  Behan DP,  Chalmers DT;
XX
DR   WPI; 2003-742861/70.
DR   N-PSDB; ADC22626.
XX
PT   Creating a constitutively active version of an endogenous human G protein
PT   coupled receptor (GPCR) comprises substituting a specific amino acid in
PT   the transmembrane-6 region with a different amino acid, and testing for
PT   constitutive activity.
XX
PS   Example 1; SEQ ID NO 108; 221pp; English.
XX
CC   The invention relates to a method for treating a non-endogenous,
CC   constitutively active version of an endogenous human G protein-coupled
CC   receptor (GPCR) that has a transmembrane-6 (TM6) region and an
CC   intracellular-3 (IC3) region, by substituting a specific amino acid in
CC   the TM6 region with a different amino acid, and testing for constitutive
CC   activity. The method is useful for creating a constitutively active
CC   version of an endogenous human GPCR that comprises a transmembrane 6
CC   region and an intracellular loop 3 region. The altered human GPCR
CC   polypeptides are useful for screening test compounds for identification
CC   of inverse agonists or partial agonists of GPCR polypeptides, which may
CC   have therapeutic uses. The altered GPCRs may also be used in vivo or in
CC   vitro in biological research. A nucleic acid encoding the altered GPCR
CC   may be used to create a transgenic animal expressing the altered GPCR.
CC   The method allows screening for compounds that modulate the activity of a
CC   human G protein-coupled receptor without the need for provision of a
CC   ligand for the receptor. This is particularly useful in allowing
CC   screening of compounds against orphan receptors for which no ligand is
CC   currently known. This sequence represents a human GPCR polypeptide of the
CC   invention.
XX
SQ   Sequence 387 AA;

  Query Match             95.6%;  Score 1990;  DB 7;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 1.7e-197;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
                 ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 15
ADH14100
ID   ADH14100 standard; protein; 387 AA.
XX
AC   ADH14100;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human HM74.
XX
KW   human; non-endogenous; G protein-coupled receptor; GPCR; receptor.
XX
OS   Homo sapiens.
XX
PN   US2003105292-A1.
XX
PD   05-JUN-2003.
XX
PF   20-SEP-2002; 2002US-00251385.
XX
PR   26-JUN-1998;   98US-0090783P.
PR   07-AUG-1998;   98US-0095677P.
PR   13-OCT-1998;   98US-00170496.
XX
PA   (LIAW/) LIAW C W.
PA   (BEHA/) BEHAN D P.
PA   (CHAL/) CHALMERS D T.
XX
PI   Liaw CW,  Behan DP,  Chalmers DT;
XX
DR   WPI; 2003-801247/75.
DR   N-PSDB; ADH14099.
XX
PT   New constitutively active, non-endogenous version of an endogenous human
PT   G protein-coupled receptor for the identification of therapeutic
PT   compounds, such as agonists.
XX
PS   Example 1; SEQ ID NO 108; 227pp; English.
XX
CC   The invention relates to a constitutively active, non-endogenous version
CC   of an endogenous human G protein-coupled receptor (GPCR). The GPCR is
CC   used for screening therapeutic compounds as inverse agonists, agonists or
CC   partial agonists. The GPCR can be also be used to elucidate and
CC   understand the roles of GPCRs in normal and diseased humans. The GPCR
CC   need not be purified and isolated to be used to screen for therapeutic
CC   compounds. The utility of the GPCR as a research tool is enhanced because
CC   the role of a particular receptor can be understood before the endogenous
CC   ligand is identified. The present sequence is used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 387 AA;

  Query Match             95.6%;  Score 1990;  DB 7;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 1.7e-197;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
                ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
                ||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
                |||||||||||||||||| ||||||||||||:|||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
                ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
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Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query % Match	Length	DB	ID	Description
1	2081	100.0	387	18	US-10-800-249-2	Sequence 2, Appli
2	1996	95.9	387	10	US-09-930-334-2	Sequence 2, Appli
3	1996	95.9	387	15	US-10-619-141-2	Sequence 2, Appli
4	1995	95.9	387	15	US-10-295-027-224	Sequence 224, App
5	1995	95.9	387	15	US-10-188-832-108	Sequence 108, App
6	1995	95.9	625	17	US-10-505-486-86	Sequence 86, Appl
7	1990	95.6	387	9	US-09-944-807-21	Sequence 21, Appl
8	1990	95.6	387	14	US-10-092-135-8	Sequence 8, Appli
9	1990	95.6	387	14	US-10-251-385-108	Sequence 108, App
10	1990	95.6	387	14	US-10-240-842-4	Sequence 4, Appli
11	1990	95.6	387	14	US-10-225-567A-281	Sequence 281, App
12	1990	95.6	387	14	US-10-296-223-4	Sequence 4, Appli
13	1990	95.6	387	14	US-10-348-083-3	Sequence 3, Appli
14	1990	95.6	387	14	US-10-044-643-43	Sequence 43, Appl
15	1990	95.6	387	15	US-10-295-027-228	Sequence 228, App
16	1990	95.6	387	16	US-10-314-048A-135	Sequence 135, App
17	1990	95.6	387	16	US-10-789-241-6	Sequence 6, Appli
18	1990	95.6	387	16	US-10-874-015-21	Sequence 21, Appl
19	1990	95.6	387	17	US-10-897-815-135	Sequence 135, App
20	1990	95.6	387	18	US-10-930-662-135	Sequence 135, App
21	1990	95.6	387	18	US-10-800-249-3	Sequence 3, Appli
22	1988	95.5	387	14	US-10-251-385-222	Sequence 222, App
23	1935	93.0	363	14	US-10-321-807-36	Sequence 36, Appl
24	1935	93.0	363	15	US-10-295-027-226	Sequence 226, App
25	1935	93.0	363	15	US-10-292-798-668	Sequence 668, App
26	1935	93.0	363	16	US-10-321-807-36	Sequence 36, Appl
27	1935	93.0	363	16	US-10-314-048A-36	Sequence 36, Appl
28	1935	93.0	363	17	US-10-897-815-36	Sequence 36, Appl
29	1935	93.0	363	18	US-10-930-662-36	Sequence 36, Appl
30	1935	93.0	363	18	US-10-800-249-4	Sequence 4, Appli
31	1930	92.7	363	10	US-09-930-334-16	Sequence 16, Appl
32	1930	92.7	363	15	US-10-619-141-16	Sequence 16, Appl
33	1921	92.3	363	16	US-10-314-048A-159	Sequence 159, App
34	1921	92.3	363	17	US-10-897-815-159	Sequence 159, App
35	1921	92.3	363	18	US-10-930-662-159	Sequence 159, App
36	1871	89.9	363	16	US-10-484-788-12	Sequence 12, Appl
37	1864	89.6	392	14	US-10-017-161-808	Sequence 808, App
38	1858	89.3	364	14	US-10-017-161-766	Sequence 766, App
39	1717	82.5	339	14	US-10-188-149A-4	Sequence 4, Appli
40	1670	80.2	363	16	US-10-484-788-14	Sequence 14, Appl
41	1591	76.5	360	16	US-10-484-788-10	Sequence 10, Appl
42	1577	75.8	360	14	US-10-044-643-44	Sequence 44, Appl
43	1577	75.8	360	16	US-10-314-048A-137	Sequence 137, App
44	1577	75.8	360	16	US-10-484-788-8	Sequence 8, Appli
45	1577	75.8	360	17	US-10-897-815-137	Sequence 137, App

ALIGNMENTS

RESULT 1
US-10-800-249-2
; Sequence 2, Application US/10800249
; Publication No. US20050227238A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; TITLE OF INVENTION: VARIANT OF HM74, HGPRBMY74
; FILE REFERENCE: D0323 NP
; CURRENT APPLICATION NUMBER: US/10/800,249
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: U.S. 60/454,942
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-800-249-2

Query Match 100.0%; Score 2081; DB 18; Length 387;
Best Local Similarity 100.0%; Pred. No. 5e-179;
Matches 387; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
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Db         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120

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Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
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Db        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
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Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
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Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
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Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 2
US-09-930-334-2
; Sequence 2, Application US/09930334
; Publication No. US20030078218A1
; GENERAL INFORMATION:
;  APPLICANT: Gabor Jarai and Shida Yousefi
;  TITLE OF INVENTION: Inflammation related G-protein coupled receptor
;  FILE REFERENCE: 4-31553A/HO 33
;  CURRENT APPLICATION NUMBER: US/09/930,334
;  CURRENT FILING DATE:  2001-08-15
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-930-334-2

  Query Match             95.9%;  Score 1996;  DB 10;  Length 387;
  Best Local Similarity   96.1%;  Pred. No. 2.3e-171;
  Matches  372;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

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Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGTANVCISF 180

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Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
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Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
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Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
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Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 3
US-10-619-141-2
; Sequence 2, Application US/10619141
; Publication No. US20040038895A1
; GENERAL INFORMATION:
;  APPLICANT: Gabor Jarai and Shida Yousefi
;  TITLE OF INVENTION: Inflammation related G-protein coupled receptor
;  FILE REFERENCE: 4-31553A/HO 33
;  CURRENT APPLICATION NUMBER: US/10/619,141
;  CURRENT FILING DATE:  2003-07-14
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-619-141-2

  Query Match             95.9%;  Score 1996;  DB 15;  Length 387;
  Best Local Similarity   96.1%;  Pred. No. 2.3e-171;
  Matches  372;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
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Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
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Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
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Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGTANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
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Db        181 SICHTFRWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
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Db        241 VICFLPSVVVRIHIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
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Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
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Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 4
US-10-295-027-224
; Sequence 224, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
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;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 224
;    LENGTH: 387
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-295-027-224

  Query Match             95.9%;  Score 1995;  DB 15;  Length 387;
  Best Local Similarity   96.1%;  Pred. No. 2.8e-171;
  Matches  372;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
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Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
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Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

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Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
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Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
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Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
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Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

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Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 5
US-10-188-832-108
; Sequence 108, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
;  APPLICANT: Mack, David H.
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
;  TITLE OF INVENTION:  and Methods of Screening for Modulators of Bladder
;  TITLE OF INVENTION:  Cancer
;  FILE REFERENCE: 018501-002330US
;  CURRENT APPLICATION NUMBER: US/10/188,832
;  CURRENT FILING DATE:  2002-11-22
;  PRIOR APPLICATION NUMBER: US 60/302,814
;  PRIOR FILING DATE: 2001-07-03
;  PRIOR APPLICATION NUMBER: US 60/310,099
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 60/343,705
;  PRIOR FILING DATE: 2001-11-08
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/372,246
;  PRIOR FILING DATE: 2002-04-12
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
;    LENGTH: 387
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-188-832-108

  Query Match             95.9%;  Score 1995;  DB 15;  Length 387;
  Best Local Similarity   96.1%;  Pred. No. 2.8e-171;
  Matches  372;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
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Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
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Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
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Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
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Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
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Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
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RESULT 6
US-10-505-486-86
; Sequence 86, Application US/10505486
; Publication No. US20050118639A1
; GENERAL INFORMATION:
;  APPLICANT: Takeda Chemical Industries, Ltd.
;  TITLE OF INVENTION: Determination of a ligand
;  FILE REFERENCE: P03-0006PCT
;  CURRENT APPLICATION NUMBER: US/10/505,486
;  CURRENT FILING DATE:  2004-08-20
;  PRIOR APPLICATION NUMBER: JP 2002-45728
;  PRIOR FILING DATE: 2002-02-22
;  PRIOR APPLICATION NUMBER: JP 2002-213949
;  PRIOR FILING DATE: 2002-07-23
;  PRIOR APPLICATION NUMBER: JP 2002-298237
;  PRIOR FILING DATE: 2002-10-11
;  NUMBER OF SEQ ID NOS: 233
; SEQ ID NO 86
;    LENGTH: 625
;    TYPE: PRT
;    ORGANISM: Human
US-10-505-486-86
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  Query Match           95.9%;  Score 1995;  DB 17;  Length 625;
  Best Local Similarity  96.1%;  Pred. No. 5e-171;
  Matches  372;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
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Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
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Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWKFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
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Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 7
US-09-944-807-21
; Sequence 21, Application US/09944807
; Patent No. US20020119494A1
; GENERAL INFORMATION:
;  APPLICANT: Boehringer Ingelheim Pharma KG
;  TITLE OF INVENTION: Method for identifying substances which positively
;  TITLE OF INVENTION:  influence inflammatory conditions of chronic
;  TITLE OF INVENTION:  inflammatory airway diseases
;  FILE REFERENCE: 082_00n
;  CURRENT APPLICATION NUMBER: US/09/944,807
;  CURRENT FILING DATE:  2001-08-31
;  PRIOR APPLICATION NUMBER: UK 0021484.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-944-807-21

  Query Match           95.6%;  Score 1990;  DB 9;  Length 387;
  Best Local Similarity  95.9%;  Pred. No. 8e-171;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| || |||||||:||| ||||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 8
US-10-092-135-8
; Sequence 8, Application US/10092135
; Publication No. US20030054374A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR,
;  TITLE OF INVENTION:  HGPRBMY27
;  FILE REFERENCE: D0134.NP
;  CURRENT APPLICATION NUMBER: US/10/092,135
;  CURRENT FILING DATE:  2002-03-06
;  PRIOR APPLICATION NUMBER: US 60/273,808
;  PRIOR FILING DATE: 2001-03-07
;  PRIOR APPLICATION NUMBER: US 60/278,983
;  PRIOR FILING DATE: 2001-03-27
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-10-092-135-8

  Query Match           95.6%;  Score 1990;  DB 14;  Length 387;
  Best Local Similarity  95.9%;  Pred. No. 8e-171;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| || |||||||:||| ||||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 9
US-10-251-385-108
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```
; Sequence 108, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
;  TITLE OF INVENTION:  Protein-Coupled
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/10/251,385
;  CURRENT FILING DATE:  2002-09-20
;  PRIOR APPLICATION NUMBER: US/09/170,496
;  PRIOR FILING DATE: 1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-251-385-108

  Query Match            95.6%;  Score 1990;  DB 14;  Length 387;
  Best Local Similarity  95.9%;  Pred. No. 8e-171;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 10
US-10-240-842-4
; Sequence 4, Application US/10240842
; Publication No. US20030109673A1
; GENERAL INFORMATION:
;  APPLICANT: Xiao, Yonghong
;  TITLE OF INVENTION: REGULATION OF HUMAN HM74-LIKE G PROTEIN-COUPLED RECEPTOR
;  FILE REFERENCE: 4974.00883
;  CURRENT APPLICATION NUMBER: US/10/240,842
;  CURRENT FILING DATE:  2002-10-04
;  PRIOR APPLICATION NUMBER: 60/194,701
;  PRIOR FILING DATE: 2000-04-05
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-240-842-4

  Query Match            95.6%;  Score 1990;  DB 14;  Length 387;
  Best Local Similarity  95.9%;  Pred. No. 8e-171;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 11
US-10-225-567A-281
; Sequence 281, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
;  APPLICANT: LifeSpan Biosciences
;  APPLICANT:  Brown, Joseph P.
;  APPLICANT:  Burmer, Glenna C.
;  APPLICANT:  Roush, Christine L.
;  TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
;  FILE REFERENCE: 1920-4-4
;  CURRENT APPLICATION NUMBER: US/10/225,567A
;  CURRENT FILING DATE:  2001-12-19
;  PRIOR APPLICATION NUMBER: 60/257,144
;  PRIOR FILING DATE: 2000-12-19
;  NUMBER OF SEQ ID NOS: 2292
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 281
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-225-567A-281

  Query Match            95.6%;  Score 1990;  DB 14;  Length 387;
  Best Local Similarity  95.9%;  Pred. No. 8e-171;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||||| |||||||||||:||||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180
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Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              |||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 12
US-10-296-223-4
; Sequence 4, Application US/10296223
; Publication No. US20030139343A1
; GENERAL INFORMATION:
;  APPLICANT: Bayer AG
;  APPLICANT:  Bull, Christof
;  TITLE OF INVENTION: REGULATION OF HUMAN HM74-LIKE G PROTEIN COUPLED RECEPTOR
;  FILE REFERENCE: Lio 080 foreign countries
;  CURRENT APPLICATION NUMBER: US/10/296,223
;  CURRENT FILING DATE:  2002-12-04
;  PRIOR APPLICATION NUMBER: 60/208,912
;  PRIOR FILING DATE: 2000-06-05
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-296-223-4

  Query Match             95.6%;  Score 1990;  DB 14;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 8e-171;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||| ||||||||||:|||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              |||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 13
US-10-348-083-3
; Sequence 3, Application US/10348083
; Publication No. US20030186873A1
; GENERAL INFORMATION:
;  APPLICANT: EISHINGDRELO, Haifeng
;  APPLICANT:  CAI, Jidong
;  APPLICANT:  SANDRASAGRA, Anthony
;  TITLE OF INVENTION: NUCLEIC ACID ENCODING A G-PROTEIN COUPLED RECEPTOR, AND USES THERI
;  FILE REFERENCE: USAV2001/0054 US NP
;  CURRENT APPLICATION NUMBER: US/10/348,083
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US 06/351,001
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: GB 0210597.1
;  PRIOR FILING DATE: 2002-05-09
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-348-083-3

  Query Match             95.6%;  Score 1990;  DB 14;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 8e-171;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db          1 MNRHHLQDHFLEIDKKNCCVFRDDFIAKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60

Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
              |||||||||||||||||||:|| |||| || ||||||||:||| ||||||||||||||
Db         61 SSRIFLFNLAVADFLLIICLPFVMDYYVRRSDWNFGDIPCRLVLFMFAMNRQGSIIFLTV 120

Qy        121 VAVDRYFRVVHPHHALNKISNRTAAIISCLLWGITIGLTVHLLKKKMPIQNGGANLCSSF 180
              |||||||||||||||||| ||||||||||:|||||||: |||| ||:| ||
Db        121 VAVDRYFRVVHPHHALNKISNWTAAIISCLLWGITVGLTVHLLKKKLLIQNGPANVCISF 180

Qy        181 SICHTFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240
              ||||||:|||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              |||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 14
US-10-044-643-43
; Sequence 43, Application US/10044643
; Publication No. US20030195335A1
; GENERAL INFORMATION:
;  APPLICANT: Majumder, Kumud
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Wolenc, Adam R
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Mishnu, Vishun S
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Spytek, Kimberly A
;  APPLICANT:  Li, Li
;  APPLICANT:  Baumgartner, Jason C
;  APPLICANT:  Gusev, Vladimir
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;  TITLE OF INVENTION: No. US20030195335A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 15966-748
;  CURRENT APPLICATION NUMBER: US/10/044,643
;  CURRENT FILING DATE:  2002-01-11
;  PRIOR APPLICATION NUMBER: 60/193,664
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: 60/194,614
;  PRIOR FILING DATE: 2000-04-05
;  PRIOR APPLICATION NUMBER: 60/195,063
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,066
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,067
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,068
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,069
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,070
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/195,510
;  PRIOR FILING DATE: 2000-04-06
;  PRIOR APPLICATION NUMBER: 60/219,855
;  PRIOR FILING DATE: 2000-07-21
;  PRIOR APPLICATION NUMBER: 60/221,284
;  PRIOR FILING DATE: 2000-07-27
;  PRIOR APPLICATION NUMBER: 60/221,325
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 60/224,588
;  PRIOR FILING DATE: 2000-08-11
;  PRIOR APPLICATION NUMBER: 60/239,613
;  PRIOR FILING DATE: 2000-10-11
;  PRIOR APPLICATION NUMBER: 60/262,508
;  PRIOR FILING DATE: 2001-01-18
;  PRIOR APPLICATION NUMBER: 60/263,604
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/263,433
;  PRIOR FILING DATE: 2001-01-23
;  PRIOR APPLICATION NUMBER: 60/265,161
;  PRIOR FILING DATE: 2001-01-30
;  NUMBER OF SEQ ID NOS: 83
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-044-643-43

  Query Match             95.6%;  Score 1990;  DB 14;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 8e-171;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

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RESULT 15
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; Sequence 228, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 228
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-295-027-228

  Query Match             95.6%;  Score 1990;  DB 15;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 8e-171;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

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Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
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Job time : 4755 secs

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OM protein - protein search, using sw model

Run on: October 20, 2005, 06:00:16 ; Search time 22 Seconds
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Title: US-10-800-249-2
Perfect score: 2081
Sequence: 1 MNRHHLQDHFLEIDKKNCCV.....KGHCHQEPASLEKQLGCCIE 387

Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1990	95.6	387	4	US-09-170-496D-108	Sequence 108, App
2	1990	95.6	387	4	US-09-944-807-21	Sequence 21, Appl
3	1988	95.5	387	4	US-09-170-496D-222	Sequence 222, App
4	563	27.1	423	2	US-08-955-713-2	Sequence 2, Appli
5	559	26.9	476	2	US-08-955-713-4	Sequence 4, Appli
6	497.5	23.9	319	3	US-09-130-749-2	Sequence 2, Appli
7	497.5	23.9	319	3	US-09-130-749-2	Sequence 2, Appli
8	494.5	23.8	319	4	US-09-170-496D-60	Sequence 60, Appl
9	494.5	23.8	319	4	US-09-170-496D-196	Sequence 196, App
10	427	20.5	362	3	US-08-513-974B-374	Sequence 374, App
11	415	19.9	373	2	US-08-559-524A-4	Sequence 4, Appli
12	415	19.9	373	3	US-08-749-707-4	Sequence 4, Appli
13	415	19.9	373	4	US-09-947-922-4	Sequence 4, Appli
14	407	19.6	373	4	US-09-745-842-14	Sequence 14, Appl
15	375.5	18.0	309	3	US-09-422-869-20	Sequence 20, Appl
16	370.5	17.8	346	4	US-09-585-876-2	Sequence 2, Appli
17	368	17.7	374	4	US-09-745-842-15	Sequence 15, Appl
18	353.5	17.0	370	3	US-08-781-250-2	Sequence 2, Appli
19	350.5	16.8	364	4	US-08-148-708-2	Sequence 2, Appli
20	350	16.8	339	1	US-08-153-848-44	Sequence 44, Appl
21	350	16.8	339	2	US-08-812-871-3	Sequence 3, Appli
22	350	16.8	339	3	US-09-299-843A-44	Sequence 44, Appl
23	350	16.8	339	3	US-09-088-337B-44	Sequence 44, Appl
24	350	16.8	339	4	US-09-170-496D-32	Sequence 32, Appl
25	350	16.8	339	5	PCT-US93-11153-44	Sequence 44, Appl
26	350	16.8	339	5	PCT-US95-07180-2	Sequence 2, Appli
27	348.5	16.7	391	4	US-09-826-509-463	Sequence 463, App
28	344	16.5	339	4	US-09-170-496D-182	Sequence 182, App
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30	343.5	16.5	302	3	US-08-467-947A-30	Sequence 30, Appl
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44	341	16.4	399	1	US-08-472-840-61	Sequence 61, Appl
45	341	16.4	399	2	US-08-476-976-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-09-170-496D-108
; Sequence 108, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-108

Query Match 95.6%; Score 1990; DB 4; Length 387;
Best Local Similarity 95.9%; Pred. No. 1.1e-164;
Matches 371; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

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Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
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Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
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Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 2
US-09-944-807-21
; Sequence 21, Application US/09944807
; Patent No. 6773895
; GENERAL INFORMATION:
;  APPLICANT: Boehringer Ingelheim Pharma KG
;  TITLE OF INVENTION: Method for identifying substances which positively
;  TITLE OF INVENTION:  influence inflammatory conditions of chronic
;  TITLE OF INVENTION:  inflammatory airway diseases
;  FILE REFERENCE: 082_00n
;  CURRENT APPLICATION NUMBER: US/09/944,807
;  CURRENT FILING DATE:  2001-08-31
;  PRIOR APPLICATION NUMBER: UK 0021484.1
;  PRIOR FILING DATE: 2000-09-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-944-807-21

  Query Match             95.6%;  Score 1990;  DB 4;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 1.1e-164;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MNRHHLQDHFLEIDKKNCCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWK 60
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Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
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Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
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RESULT 3
US-09-170-496D-222
; Sequence 222, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-222

  Query Match             95.5%;  Score 1988;  DB 4;  Length 387;
  Best Local Similarity   95.9%;  Pred. No. 1.6e-164;
  Matches  371;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

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Qy         61 SSRIFLFNLAVADFLLIICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTV 120
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Db        181 SICHTFRWHEAMFLLEFLLPLGIILFCSARIIWSLRQRQMDRHAKIKRAKTFIMVVAIVF 240

Qy        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VICFLPSVVVRIRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPS 300

Qy        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 FPNFFSTLINRCLQRKMTGEPDNNRSTSVELTGDPNKTRGAPEALMANSGEPWSPSYLGP 360

Qy        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387
              ||||||||||||||||||||||||||||
Db        361 TSNNHSKKGHCHQEPASLEKQLGCCIE 387


RESULT 4
US-08-955-713-2
; Sequence 2, Application US/08955713
; Patent No. 5955308
;  GENERAL INFORMATION:
;    APPLICANT:  SATHE, GANESH
;    APPLICANT:  MOONEY, JEFFREY
;    APPLICANT:  BERGSMA, DERK
;    APPLICANT:  HALSEY, WENDY
;    TITLE OF INVENTION:  cDNA CLONE HEOAD54 THAT ENCODES        A HUMAN 7-TRANS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/955,713
;      FILING DATE:  23-OCT-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/050,124
;      FILING DATE:  18-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
```

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;      REFERENCE/DOCKET NUMBER:  GH-70087
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  423 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-955-713-2
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Query Match 27.1%; Score 563; DB 2; Length 423;
Best Local Similarity 41.8%; Pred. No. 6.7e-41;
Matches 118; Conservative 52; Mismatches 88; Indels 24; Gaps 5;

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Qy         30 LPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVR 89
Db         95 LAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFLLISNLPLRVDYYLL 154

Qy         90 RWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISC 149
Db        155 HETWRFGAAACKVNLFMLSTNRTASVVFLTAIALNRYLKVVQPHHVLSRASVGAAARVAG 214

Qy        150 LLWGITIGLTVHLLKKKMPIQNGGANLCSSFSI----CHTFQWHEAMFLLEFFLPLGIIL 205
Db        215 GLWVGILLLNGHLL-----LSTFSGPSCLSYRVGTKPSASLRWHQALYLLEFFLPLALIL 269

Qy        206 FCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVV---VRIRIFWLLHTSG 262
Db        270 FAIVSIGLTIRNRGLGGQAGPQRAMRVLAMVVAVYTICFLPSIIFGMASMVAFWL----- 324

Qy        263 TQNCEVYRSVDLA---FFITLSFTYMNSMLDPVVYYFSSPSF 301
Db        325 ----SACRSLDLCTQLFHGSLAFTYLNSVLDPVLYCFSSPNF 362
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RESULT 5
US-08-955-713-4
; Sequence 4, Application US/08955713
; Patent No. 5955308
;  GENERAL INFORMATION:
;    APPLICANT:  SATHE, GANESH
;    APPLICANT:  MOONEY, JEFFREY
;    APPLICANT:  BERGSMA, DERK
;    APPLICANT:  HALSEY, WENDY
;    TITLE OF INVENTION:  cDNA CLONE HEOAD54 THAT ENCODES        A HUMAN 7-TRANS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY, FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/955,713
;      FILING DATE:  23-OCT-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/050,124
;      FILING DATE:  18-JUN-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-70087
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  476 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-955-713-4
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Query Match 26.9%; Score 559; DB 2; Length 476;
Best Local Similarity 41.5%; Pred. No. 1.7e-40;
Matches 117; Conservative 53; Mismatches 88; Indels 24; Gaps 6;

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Qy         30 LPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVR 89
Db          6 LAPILALEFVLGLVGNSLALFIFCIHTRPWTSNTVFLVSLVAADFLLISNLPLRVDYYLL 65

Qy         90 RWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISC 149
Db         66 HETWRFGAAACKVNLFMLSTNRKASVVFLTAIALNRYLKVVXPHHVLNRASVGAXARVX- 124

Qy        150 LLWGITIGLTVHLLKKKMPIQNGGANLCSSFSI----CHTFQWHEAMFLLEFFLPLGIIL 205
Db        125 --GGIWVGIL--LLNGXLLLNTFSGPSCLSYRVGTKPSASLRWHQALYLLEFFLPLALIL 180

Qy        206 FCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVV---VRIRIFWLLHTSG 262
Db        181 FAIVSIGLTIRNRGLGGQAGPQRAMRVLAMVVAVYTICFLPSIIFGMASMVAFWL----- 235

Qy        263 TQNCEVYRSVDLA---FFITLSFTYMNSMLDPVVYYFSSPSF 301
Db        236 ----SACRSLDLCTQLFHGSLAFTYLNSVLDPVLYCFSSPNF 273
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RESULT 6
US-09-130-749-2
; Sequence 2, Application US/09130749
; Patent No. 6031090
;  GENERAL INFORMATION:
;       APPLICANT: SHABON, USMAN
;                  ELSHOURBAGY, NABIL
;       TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM
;                           RECEPTOR (GPR31A)
;       NUMBER OF SEQUENCES: 2
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: RATNER & PRESTIA
;            STREET: P.O. Box 980
;            CITY: Valley Forge
;            STATE: PA
;            COUNTRY: USA
;            ZIP: 19482
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/130,749
;            FILING DATE: 07-Aug-1998
;            CLASSIFICATION: UNKNOWN
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: <Unknown>
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: PRESTIA, PAUL F
;            REGISTRATION NUMBER: 23,031
;            REFERENCE/DOCKET NUMBER: GP-70513
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 610-407-0700
```

```
;            TELEFAX: 610-407-0701
;            TELEX: 846169
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 319 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-130-749-2

  Query Match            23.9%;  Score 497.5;  DB 3;  Length 319;
  Best Local Similarity  36.4%;  Pred. No. 2.3e-35;
  Matches  110;  Conservative   56;  Mismatches  111;  Indels   25;  Gaps    5;

Qy         33 VLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRWD 92
              :||||   ||||| :||| | | :: ||   ::| |||:|| ||  |||||   |:
Db         20 LLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAACLPFLAAFYLSLQA 79

Qy         93 WKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLW 152
              |  | : |  : |:| ::|   : ||  ||:||| |||||   :| :| : |  :| |:|
Db         80 WHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNLLSPQAALGVSGLVW 139

Qy        153 GITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQ----------WHEAMFLLEFFLPLG 202
               : : ||   |       ||         : ||:|           | ||:  |:| || |
Db        140 LLMVALTCPGLLISEAAQNS--------TRCHSFYSRADGSFSIIWQEALSCLQFVLPFG 191

Qy        203 IILFCSARIIWSL--RQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLHT 260
              :|:||:| || :|  | |: ::  |::||   : :| ::| :||||  : |:    |:|
Db        192 LIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLARV----LMHI 247

Qy        261 -SGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQRKMTG 319
                   :|    :|     :| | ||::|:|:|||| ||||:| : :  : :    :
Db        248 FQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRVFHTLRGKGQAA 307

Qy        320 EP 321
              ||
Db        308 EP 309


RESULT 7
US-09-130-749-2
; Sequence 2, Application US/09130749
; Patent No. 6031344
;  GENERAL INFORMATION:
;    APPLICANT:  SHABON, USMAN
;    APPLICANT:  ELSHOURBAGY, NABIL
;    TITLE OF INVENTION:  MOLECULAR CLONING OF A 7TM
;    TITLE OF INVENTION:  RECEPTOR (GPR31A)
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. Box 980
;      CITY:  Valley Forge
;      STATE:  PA
;      COUNTRY:  USA'
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/130,749
;      FILING DATE:  07-AUG-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GP-70513
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  319 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-130-749-2

  Query Match            23.9%;  Score 497.5;  DB 3;  Length 319;
  Best Local Similarity  36.4%;  Pred. No. 2.3e-35;
  Matches  110;  Conservative   56;  Mismatches  111;  Indels   25;  Gaps    5;

Qy         33 VLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRWD 92
              :||||   ||||| :||| | | :: ||   ::| |||:|| ||  |||||   |:
Db         20 LLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAACLPFLAAFYLSLQA 79

Qy         93 WKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLW 152
              |  | : |  : |:| ::|   : ||  ||:||| |||||   :| :| : |  :| |:|
Db         80 WHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNLLSPQAALGVSGLVW 139

Qy        153 GITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQ----------WHEAMFLLEFFLPLG 202
               : : ||   |       ||         : ||:|           | ||:  |:| || |
Db        140 LLMVALTCPGLLISEAAQNS--------TRCHSFYSRADGSFSIIWQEALSCLQFVLPFG 191

Qy        203 IILFCSARIIWSL--RQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLHT 260
              :|:||:| || :|  | |: ::  |::||   : :| ::| :||||  : |:    |:|
Db        192 LIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLARV----LMHI 247

Qy        261 -SGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQRKMTG 319
                   :|    :|     :| | ||::|:|:|||| ||||:| : :  : :    :
Db        248 FQNLGSCRALCAVAHTSDVTGSLTYLHSVLNPVVYCFSSPTFRSSYRRVFHTLRGKGQAA 307

Qy        320 EP 321
              ||
Db        308 EP 309


RESULT 8
US-09-170-496D-60
; Sequence 60, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-C
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
;   LENGTH: 319
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-60

  Query Match            23.8%;  Score 494.5;  DB 4;  Length 319;
  Best Local Similarity  36.1%;  Pred. No. 4.3e-35;
  Matches  109;  Conservative   57;  Mismatches  111;  Indels   25;  Gaps    5;

Qy         33 VLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRWD 92
              :||||   ||||| :||| | | :: ||   ::| |||:|| ||  |||||   |:
Db         20 LLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAACLPFLAAFYLSLQA 79

Qy         93 WKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLW 152
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Db         80 WHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNLLSPQAALGVSGLVW 139

Qy        153 GITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQ----------WHEAMFLLEFFLPLG 202

Db        140 LLMVALTCPGLLISEAAQNS--------TRCHSFYSRADGSFSIIWQEALSCLQFVLPFG 191

Qy        203 IILFCSARIIWSL--RQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLHT 260

Db        192 LIVFCNAGIIRALQKRLREPEKQPKLQRAQALVTLVVVLFALCFLPCFLARV----LMHI 247

Qy        261 -SGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQRKMTG 319

Db        248 FQNLGSCRALCAVAHTSDVTGSLTYLHSVVNPVVYCFSSPTFRSSYRRVFHTLRGKGQAA 307

Qy        320 EP 321

Db        308 EP 309


RESULT 9
US-09-170-496D-196
; Sequence 196, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
;  APPLICANT: Behan, Dominic P.
;  APPLICANT:  Chalmers, Derek T.
;  APPLICANT:  Liaw, Chen W.
;  TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
;  TITLE OF INVENTION:  Receptors
;  FILE REFERENCE: AREN-0040
;  CURRENT APPLICATION NUMBER: US/09/170,496D
;  CURRENT FILING DATE:  1998-10-13
;  NUMBER OF SEQ ID NOS: 294
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
;   LENGTH: 319
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-170-496D-196

  Query Match            23.8%;  Score 494.5;  DB 4;  Length 319;
  Best Local Similarity  36.1%;  Pred. No. 4.3e-35;
  Matches  109;  Conservative   57;  Mismatches  111;  Indels   25;  Gaps    5;

Qy         33 VLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRWD 92

Db         20 LLGLECGLGLLGNAVALWTFLFRVRVWKPYAVYLLNLALADLLLAACLPFLAAFYLSLQA 79

Qy         93 WKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLW 152

Db         80 WHLGRVGCWALRFLLDLSRSVGMAFLAAVALDRYLRVVHPRLKVNLLSPQAALGVSGLVW 139

Qy        153 GITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQ----------WHEAMFLLEFFLPLG 202

Db        140 LLMVALTCPGLLISEAAQNS--------TRCHSFYSRADGSFSIIWQEALSCLQFVLPFG 191

Qy        203 IILFCSARIIWSL--RQRQMDRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLHT 260

Db        192 LIVFCNAGIIRALQKRLREPEKQPKLQRAKALVTLVVVLFALCFLPCFLARV----LMHI 247

Qy        261 -SGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPNFFSTLINRCLQRKMTG 319

Db        248 FQNLGSCRALCAVAHTSDVTGSLTYLHSVVNPVVYCFSSPTFRSSYRRVFHTLRGKGQAA 307

Qy        320 EP 321

Db        308 EP 309


RESULT 10
US-08-513-974B-374
; Sequence 374, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-007177
;      FILING DATE:  20-JAN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-326611
;      FILING DATE:  28-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-270017
;      FILING DATE:  02-NOV-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236357
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-236356
;      FILING DATE:  30-SEP-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189274
;      FILING DATE:  11-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189273
;      FILING DATE:  11-AUG-1945
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 6-189272
;      FILING DATE:  11-AUG-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resnick, David S.
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  45753
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;  INFORMATION FOR SEQ ID NO:  374:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  362 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  peptide
US-08-513-974B-374

  Query Match           20.5%;  Score 427;  DB 3;  Length 362;
  Best Local Similarity   29.4%;  Pred. No. 3.5e-29;
  Matches   97;  Conservative   73;  Mismatches  132;  Indels   28;  Gaps    8;

Qy         18 CCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLI 77
              | : :  |     || |  | || | ||| :|:|:| ||:: |    :::||||:|||| :
Db         31 CSLTKTGFQFYYLPTVYILVFITGFLGNSVAIWMFVFHMRPWSGISVYMFNLALADFLYV 90

Qy         78 ICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALN 137
              : || |:  |  : || |||: |:|  |:  :|  |||:||| ::| ||  |||| :|
Db         91 LTLPALIFYYFNKTDWIFGDVMCKLQRFIFHVNLYGSILFLTCISVHRYTGVVHPLKSLG 150

Qy        138 KISNRTAAIISCLLWGITIGLTVHLL-KKKMPIQNGGANLCSS------------FSICH 184
              ::  : |  :| |:| : : :   :|    : ::      |              :|:|
Db        151 RLKKKNAVYVSSLVWALVVAVIAPILFYSGIGVRRNKTITCYDTTADEYLRSYFVYSMCT 210

Qy        185 TFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAI-VFVIC 243
              |          :  | :|  :|| |   |: :|  : :| :: ::|  |::::: : || :
Db        211 T--------VFMFCIPFIVILGCYGLIVKALIYKDLD-NSPLRRKSTYLVIIVLTVFAVS 261

Qy        244 FLPSVVVR-IRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFP 302
              :||  |:: : :   |     | |     |   : :|    :|| :||::|: :  :|
Db        262 YLPFHVMKTLNLRARLDFQTPQMCAFNDKVYATYQVTRGLASLNSCVDPILYFLAGDTFR 321

Qy        303 NFFSTLINRCLQRKMTGEPDNNRSTSVELT 332
                |    :  :|    || | :| | |:|
Db        322 RRLSRATRKSSRR---SEP-NVQSKSEEMT 347


RESULT 11
US-08-559-524A-4
; Sequence 4, Application US/08559524A
; Patent No. 5871963
;  GENERAL INFORMATION:
;    APPLICANT:  Conley, Pamela B.
;    APPLICANT:  Jantzen, Hans-Michael
;    TITLE OF INVENTION:  NOVEL PURINERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN, LEWIS & BOCKIUS LLP
;      STREET:  1800 M Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5869
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/559,524A
;      FILING DATE:  15-NOV-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Adler, Reid G.
;      REGISTRATION NUMBER:  30,988
;      REFERENCE/DOCKET NUMBER:  044481-5010-00-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-7000
;      TELEFAX:  202-467-7176
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  373 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-559-524A-4

  Query Match           19.9%;  Score 415;  DB 2;  Length 373;
  Best Local Similarity   29.8%;  Pred. No. 4e-28;
  Matches   98;  Conservative   66;  Mismatches  139;  Indels   26;  Gaps    6;

Qy         18 CCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLI 77
              | : :  |     || |  | || | ||| :|:|:| ||:| |    :::||||:|||| :
Db         42 CALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYV 101

Qy         78 ICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALN 137
              : || |:  |  : || |||  |:|  |:  :|  |||:||| ::  ||  ||:|  :|
Db        102 LTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLG 161

Qy        138 KISNRTAAIISCLLWGI-TIGLTVHLLKKKMPIQNGGANLCSS------------FSICH 184
              ::  : |  || |:| |  :|::  |       |:       |              :|:|
Db        162 RLKKKNAVYISVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSMCT 221

Qy        185 TFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICF 244
              |      |||     :|| :|| |    |: :|  : :|     :::|  :::|  || : :
Db        222 TV----AMFC----VPLVLILGCYGLIVRALIYKDLDNSPLRRKSIYLVIIVLTVFAVSY 273

Qy        245 LPSVVVR-IRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPN 303
              :|  |:: : :   |     : |     |   : :|     :|| :||::|: :  :|
Db        274 IPFHVMKTMNLRARLDFQTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR 333

Qy        304 FFSTLINRCLQRKMTGEPDNNRSTSVELT 332
                |    :  :|       | :| | ::|
Db        334 RLSRATRKASRRSEA----NLQSKSEDMT 358


RESULT 12
US-08-749-707-4
; Sequence 4, Application US/08749707
; Patent No. 6063582
;  GENERAL INFORMATION:
;    APPLICANT:  Conley, Pamela B.
;    APPLICANT:  Jantzen, Hans-Michael
;    TITLE OF INVENTION:  NOVEL PURINERGIC RECEPTOR
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN, LEWIS & BOCKIUS LLP
;      STREET:  1800 M Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20036-5869
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/749,707
;      FILING DATE:  15-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Adler, Reid G.
;      REGISTRATION NUMBER:  30,988
;      REFERENCE/DOCKET NUMBER:  044481-5010-01-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-467-7000
;      TELEFAX:  202-467-7176
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  373 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-749-707-4

  Query Match           19.9%;  Score 415;  DB 3;  Length 373;
  Best Local Similarity   29.8%;  Pred. No. 4e-28;
  Matches   98;  Conservative   66;  Mismatches  139;  Indels   26;  Gaps    6;
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Qy         18 CCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLI 77
Db         42 CALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYV 101

Qy         78 ICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALN 137
Db        102 LTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLG 161

Qy        138 KISNRTAAIISCLLWGI-TIGLTVHLLKKKMPIQNGGANLCSS------------FSICH 184
Db        162 RLKKKNAVYISVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSMCT 221

Qy        185 TFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICF 244
Db        222 TV----AMFC----VPLVLILGCYGLIVRALIYKDLDNSPLRRKSIYLVIIVLTVFAVSY 273

Qy        245 LPSVVVR-IRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPN 303
Db        274 IPFHVMKTMNLRARLDFQTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR 333

Qy        304 FFSTLINRCLQRKMTGEPDNNRSTSVELT 332
Db        334 RLSRATRKASRRSEA----NLQSKSEDMT 358
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RESULT 13
US-09-947-922-4
; Sequence 4, Application US/09947922
; Patent No. 6680373
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/947,922
; FILING DATE: 07-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-947-922-4

Query Match 19.9%; Score 415; DB 4; Length 373;
Best Local Similarity 29.8%; Pred. No. 4e-28;
Matches 98; Conservative 66; Mismatches 139; Indels 26; Gaps 6;

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Qy         18 CCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLI 77
Db         42 CALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYV 101

Qy         78 ICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALN 137
Db        102 LTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLG 161

Qy        138 KISNRTAAIISCLLWGI-TIGLTVHLLKKKMPIQNGGANLCSS------------FSICH 184
Db        162 RLKKKNAVYISVLVWLIVVVGISPILFYSGTGIRKNKTITCYDTTSDEYLRSYFIYSMCT 221

Qy        185 TFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICF 244
Db        222 TV----AMFC----VPLVLILGCYGLIVRALIYKDLDNSPLRRKSIYLVIIVLTVFAVSY 273

Qy        245 LPSVVVR-IRIFWLLHTSGTQNCEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSFPN 303
Db        274 IPFHVMKTMNLRARLDFQTPEMCAFNDRVYATYQVTRGLASLNSCVDPILYFLAGDTFRR 333

Qy        304 FFSTLINRCLQRKMTGEPDNNRSTSVELT 332
Db        334 RLSRATRKASRRSEA----NLQSKSEDMT 358
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RESULT 14
US-09-745-842-14
; Sequence 14, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-DuBridge, Vanitha
; APPLICANT: Julius, David
; APPLICANT: Hollopeter, Gunter
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: P2Y12 Receptor
; FILE REFERENCE: 44481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P2Y1 purinergic receptor; p2yr
US-09-745-842-14

Query Match 19.6%; Score 407; DB 4; Length 373;
Best Local Similarity 28.5%; Pred. No. 2e-27;
Matches 97; Conservative 62; Mismatches 133; Indels 48; Gaps 7;

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Qy         18 CCVFRDDFIVKVLPPVLGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLI 77
Db         42 CALTKTGFQFYYLPAVYILVFIIGFLGNSVAIWMFVFHMKPWSGISVYMFNLALADFLYV 101

Qy         78 ICLPFLMDNYVRRWDWKFGDIPCRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALN 137
Db        102 LTLPALIFYYFNKTDWIFGDAMCKLQRFIFHVNLYGSILFLTCISAHRYSGVVYPLKSLG 161

Qy        138 KISNRTAAIISCLLWGI-TIGLTVHLLKKKMPIQNGGANLCSS------------FSICH 184
Db        162 RLKKKNAICISVLVWLIVVVAISPILFYSGTGVRKNKTITCYDTTSDEYLRSYFIYSMCT 221

Qy        185 TFQWHEAMFLLEFFLPLGIILFCSARIIWSLRQRQMDRHAKIKRAITFIMVVAIVFVICF 244
Db        222 TV----AMFC----VPLVLILGCYGLIVRALIYKDLDNSPLRRKSIYLVIIVLTVFAVSY 273
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Qy        245 LPSVVVRIRIFWLLHTSGTQN-----------CEVYRSVDLAFFITLSFTYMNSMLDPV 292
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Db        274 IP----------FHVMKTMNLRARLDFQTPAMCAFNDRVYATYQVTRGLASLNSCVDPI 322

Qy        293 VYYFSSPSFPNFFSTLINRCLQRKMTGEPDNNRSTSVELT 332
              :|: :  :|    |    :  :|       | :| | ::|
Db        323 LYFLAGDTFRRRLSRATRKASRRSEA----NLQSKSEDMT 358


RESULT 15
US-09-422-869-20
; Sequence 20, Application US/09422869
; Patent No. 6235481
; GENERAL INFORMATION:
;  APPLICANT: POLONSKY, KENNETH S.
;  APPLICANT: HORIKAWA, YUKIO
;  APPLICANT: ODA, NAOHISA
;  APPLICANT: COX, NANCY J.
;  APPLICANT: SREENAN, SEAMUS
;  APPLICANT: ZHOU, YUN-PING
;  APPLICANT: OTANI, KENICHI
;  APPLICANT: HANIS, CRAIG L.
;  APPLICANT: BELL, GRAEME I.
;  TITLE OF INVENTION: METHODS OF TREATMENT OF TYPE 2 DIABETES
;  FILE REFERENCE: ARCD:307
;  CURRENT APPLICATION NUMBER: US/09/422,869
;  CURRENT FILING DATE: 1999-10-21
;  EARLIER APPLICATION NUMBER: 60/134,175
;  EARLIER FILING DATE: 1999-05-13
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
;   LENGTH: 309
;   TYPE: PRT
;   ORGANISM: Human
US-09-422-869-20

  Query Match             18.0%;  Score 375.5;  DB 3;  Length 309;
  Best Local Similarity   34.1%;  Pred. No. 8.6e-25;
  Matches   94;  Conservative   48;  Mismatches  107;  Indels   27;  Gaps   10;

Qy         34 LGLEFIFGLLGNGLALWIFCFHLKSWKSSRIFLFNLAVADFLLIICLPFLMDNYVRRWDW 93
              ||:  : ||| | ||||:||  :: |  :||:: |||||  |:  |||:: :
Db         27 LGVLLVLGLLLNSLALWVFCCRMQQWTETRIYMTNLAVADLCLLCTLPFVLHSL-----R 81

Qy         94 KFGDIP-CRLMLFMLAMNRQGSIIFLTVVAVDRYFRVVHPHHALNKISNRTAAIISCLLW 152
                | | |:|   :   ||  ||  :| :|||||  | ||  |    | | || :  :||
Db         82 DTSDTPLCQLSQGIYLTNRYMSISLVTAIAVDRYVAVRHPLRARGLRSPRQAAAVCAVLW 141

Qy        153 GITIGLTVHLLKKKMPIQNGGANLCSSFSICHTFQWHEAMF-LLEFFLPLGIILFCSARI 211
               : ||  |   :  : || ||   |   | | |  :   | || |:||| :::||| ::
Db        142 VLVIGSLV--ARWLLGIQEGG--FCFR-STRHNF--NSMRFPLLGFYLPLAVVVFCSLKV 194

Qy        212 IWSLRQR---QMDRHAKIKRAITFIMVVAIVFVICFLP---SVVVRIRIFWLLHTSGTQN 265
              : :| ||    : :    ::|   :    :|||:|||    : ||: : |
Db        195 VTALAQKPPTDVGQAEATRKAARMVWANLLVFVVCFLPLHVGLTVRLAVGW-------NA 247

Qy        266 CEVYRSVDLAFFITLSFTYMNSMLDPVVYYFSSPSF 301
              | :  ::  | :||   :  |  || : ||: :  |
Db        248 CALLETIPRALYITSKLSDANCCLDAICYYYMAKEF 283


Search completed: October 20, 2005, 06:34:05
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